

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2004, 16:35:49 ; Search time 39 seconds
(without alignments)

550.134 Million cell updates/sec

Title: US-10-623-629-2

Perfect score: 379

Sequence: 1 MKVLLFAVFFCLVQRNSGD.....GDICSDPMNRCCVSSSIKNR 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rv1:*
- 16: sp_bacteriapi:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	379	100.0	68	11 Q8VBV2	Q8vbv2 rattus norv
2	341	90.0	69	11 Q8K4N2	Q8k4n2 mus musculu
3	291	76.8	80	6 Q8SOD3	Q8sqd3 macaca mula
4	286	75.5	80	4 Q9H4P9	Q9hd49 homo sapien
5	276	72.8	80	6 Q9MZ26	Q9mz26 pan troglod
6	228	60.2	82	6 Q8SQC5	Q8sqc5 macaca mula
7	75	19.8	64	6 Q97942	Q97942 capra hircu
8	75	19.8	67	11 Q7TNV9	Q7tnv9 mus musculu
9	71	18.7	29	6 Q8SOD5	Q8sqd5 macaca mula
10	69	18.2	341	11 Q8OUP9	Q8oup9 mus musculu
11	68	17.9	64	6 Q7Y843	Q7y843 bubalus bub
12	66	17.4	64	6 Q95JD2	Q95jd2 pan troglod
13	66	17.4	729	10 Q8LMU8	Q8lm8 oryza sativ
14	65.5	17.3	96	6 Q9TU00	Q9tu00 macaca mula
15	65.5	17.3	96	6 Q9TTZ9	Q9ttz9 macaca mula
16	65.5	17.3	96	6 P82318	P82318 macaca mula

17	65.5	17.3	1319	4	Q9HCD3	Q9hcd3 homo sapien
18	65	17.2	101	16	Q81KL6	Q81kl6 bacillus an
19	64.5	17.0	276	4	Q9Y417	Q9y417 homo sapien
20	64.5	17.0	375	16	Q8E982	Q8e982 shewanella
21	64	16.9	200	4	Q96Q79	Q96q79 homo sapien
22	64	16.9	233	4	Q9BU32	Q9bu32 homo sapien
23	64	16.9	239	4	Q96NT3	Q96nt3 homo sapien
24	63.5	16.8	67	11	Q8R2I6	Q8r2i6 mus musculu
25	63	16.6	139	5	Q19698	Q19698 caenorhabdi
26	63	16.6	148	13	Q90XI6	Q90xi6 amia calva
27	63	16.6	211	11	Q8BLZ0	Q8blz0 mus musculu
28	63	16.6	242	11	Q8BZ16	Q8bz16 mus musculu
29	63	16.6	281	11	Q80XN8	Q80xn8 mus musculu
30	62.5	16.5	358	5	Q9U362	Q9u362 caenorhabdi
31	62.5	16.5	393	11	Q8OVA4	Q8ova4 mus musculu
32	62.5	16.5	685	11	Q8K0I3	Q8k0i3 mus musculu
33	62.5	16.5	837	11	Q80TK2	Q80tk2 mus musculu
34	62.5	16.5	909	11	Q8SK2	Q8sk2 mus musculu
35	62.5	16.5	956	11	Q99K22	Q99k22 mus musculu
36	62	16.4	139	5	Q76358	Q76358 caenorhabdi
37	62	16.4	205	16	Q31812	Q31812 bacillus su
38	61	16.1	112	10	Q8H286	Q8h286 ananas como
39	61	16.1	4706	10	Q9FN44	Q9fn44 arabidopsis
40	60.5	16.0	364	11	Q80ZM9	Q80zm9 mus musculu
41	60.5	16.0	365	4	Q8N2E5	Q8n2e5 homo sapien
42	60	15.8	101	16	Q816T9	Q816t9 bacillus ce
43	59.5	15.7	150	11	Q8VD85	Q8vd85 rattus tiom
44	59	15.6	644	16	Q86346	Q86346 mycobacteri
45	59	15.6	644	16	Q7U0Z6	Q7u0z6 mycobacteri

ALIGNMENTS

RESULT 1

Q8VBV2

ID Q8VBV2 PRELIMINARY; PRT; 68 AA.

AC Q8VBV2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Anti-microbial-like protein BIN-1B.
GN BIN-1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Caput epididymis;
RA Li P., Shang Q., Zhang Y.D., Zhang Y.L.;
RT "Genomic DNA cloning of a rat epididymis-specific gene (Bin-1b).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Caput epididymis;
RA Li P., He B., Zhang Y.D., Zhang Y.L.;
RT "Cloning and characterization of a rat epididymis caput region-specific cDNA (Bin-1b).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL:AF217089, AAL55637.1, -;
DR EMBL:AF217089, AAL55636.1, -;
SQ SEQUENCE 68 AA; 7799 MW; 86BCC7AD52FA53E CRC64;

Query Match 100.0%; Score 379; DB 11; Length 68;

Best Local Similarity 100.0%; Pred. No. 2e-44;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRHCFMCRSGERKGDICSDPMNRCC 60

Db 1 MKVLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRHCFMCRSGERKGDICSDPMNRCC 60

QY 61 VSSSIKNR 68

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Db      61 VSSSIKXR 68
|||||
SQ SEQUENCE 80 AA; 9144 MW; F85776E60130AF98 CRC64;
Query Match 76.8%; Score 291; DB 6; Length 80;
Best Local Similarity 77.8%; Pred. No. 3e-32;
Matches 49; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

RESULT 2
Q8K4N2 PRELIMINARY; PRT; 69 AA.
AC Q8K4N2; (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE E2pe (ANTI-microbial-like protein BIN-1B homolog).
GN 9230111C06RIK OR MEP2E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis;
RX MEDLINE=22181517; PubMed=12193721;
RA Yamaguchi Y., Nagase T., Makita R., Fukuhara S., Tomita T.,
RA Tominaga T., Kurihara H., Cuchi Y.;
RT "Identification of Multiple Novel Epididymis-Specific beta-Defensin
RT Isoforms in Humans and Mice.";
RL J. Immunol. 169:2516-2523(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Epididymis;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AB089183; BAC10633.1; -
DR EMBL; AK020333; BAC25623.1; -
DR MGD; MGI:1925378; 9230111C08RIK.
SQ SEQUENCE 69 AA; 7901 MW; 635B55249FF84F49 CRC64;
Query Match 90.0%; Score 341; DB 11; Length 69;
Best Local Similarity 88.2%; Pred. No. 3.4e-39;
Matches 60; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKVLLFAVFCVQNSGDIIPGIRNTVCFMORGHCRLEFMCRSGERKGDICSDPWNRC 60
Db 1 MKVLLFAVFCVQNSGDIIPGIRNTVCFMORGHCRLEFMCRSGERKGDICSDPWNRC 60
Qy 61 VSSSIKXR 68
Db 61 VPYSVKOR 68
|||||
RESULT 3
Q8SQD3 PRELIMINARY; PRT; 80 AA.
AC Q8SQD3; (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE EP2E protein.
GN EP2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC Frohlich O., Po C., Young L.G.;
RA "EP2 splicing variants in the rhesus monkey epididymis.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466348; AAL74198.1; -
SQ SEQUENCE 80 AA; 9107 MW; CF21F5856C744019 CRC64;
Query Match 72.8%; Score 276; DB 6; Length 80;
Best Local Similarity 75.0%; Pred. No. 3.5e-30;

SQ SEQUENCE 80 AA; 9144 MW; F85776E60130AF98 CRC64;
Query Match 76.8%; Score 291; DB 6; Length 80;
Best Local Similarity 77.8%; Pred. No. 3e-32;
Matches 49; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKVLLFAVFCVQNSGDIIPGIRNTVCFMORGHCRLEFMCRSGERKGDICSDPWNRC 60
Db 1 MKVFFLFAVLFCVLRNSGDPVPPGIRNTICLMQOGTCRLFFCHSGEKKRDICSDPWNRC 60
Qy 61 VSS 63
Db 61 VSN 63
|||||
RESULT 4
Q9H4P9 PRELIMINARY; PRT; 80 AA.
AC Q9H4P9; (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE EP2E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Frohlich O., Po C., Young L.G.;
RA "Genomic organization of the human epididymal EP2 gene and its
RA relationship to defensin genes.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY005129; AAC21882.1; -
SQ SEQUENCE 80 AA; 9091 MW; CF3DE98570684019 CRC64;
Query Match 75.5%; Score 286; DB 4; Length 80;
Best Local Similarity 76.6%; Pred. No. 1.5e-31;
Matches 49; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MKVLLFAVFCVQNSGDIIPGIRNTVCFMORGHCRLEFMCRSGERKGDICSDPWNRC 60
Db 1 MKVFFLFAVLFCVLRNSGDPVPPGIRNTICRMQOGICRLFFCHSGEKKRDICSDPWNRC 60
Qy 61 VSSS 64
Db 61 VSNT 64
|||||
RESULT 5
Q9MZ26 PRELIMINARY; PRT; 80 AA.
AC Q9MZ26; (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE EP2 protein variant E.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20277601; PubMed=10819450;
RA Frohlich O., Po C., Murphy T., Young L.G.;
RA "Multiple promoter and splicing mRNA variants of the epididymis-
RA specific gene EP2.";
RL J. Androl. 21:421-430(2000).
DR EMBL; AF263555; AAF87722.1; -
SQ SEQUENCE 80 AA; 9107 MW; CF21F5856C744019 CRC64;
Query Match 72.8%; Score 276; DB 6; Length 80;
Best Local Similarity 75.0%; Pred. No. 3.5e-30;
```

	Matches	48;	Conservative	6;	Mismatches	10;	Indels	0;	Gaps	0;
QY	1	MKVLLFAVFFCLVQNSGSDIPGIRNTVCFMQRGHCRLEFMCRSGERKGDICSDPWNRC	60							
Db	1	MKVFFLFAVLFCVLQVNSGDPVLGIRNTICRMQGGICRLFFCHSGEKKRDICSDPWNRC	60							
QY	61	VSSS 64								
Db	61	VSNT 64								
RESULT 6										
O8QC5	PRELIMINARY; PRT; 82 AA.									
ID	Q8QC5	PRELIMINARY; PRT; 82 AA.								
DT	01-JUN-2002	(TrEMBLrel. 21, Created)								
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)								
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)								
DE	EP2Q protein.									
GN	EP2.									
OS	Macaca mulatta (Rhesus macaque).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;									
OC	Cercopithecoidea; Macaca.									
OX	NCBI_TaxID=9544;									
OX	[1]	NCBI_TaxID=9544;								
RN	SEQUENCE FROM N.A.									
RP	Frohlich O., Po C., Young L.G.;									
RA	"EP2 splicing variants in the rhesus monkey epididymis.";									
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.									
RL	EMBL; AF466356;	AAL74206.1; -								
DR	InterPro; IPR007988;	Sperm Ag HE2.								
DR	Pfam; PF05324;	Sperm Ag HE2; 1.								
DR	SEQUENCE	82 AA;	9329 NW;	B063D3530886314	CRC64;					
QY	4	LLPFAVFFCLVQNSGSDIPGIRNTVCFMQRGHCRLEFMCRSGERKGDICSDPWNRCVSS	63							
Db	12	LLVALLP-----PGDVPPGIRNTICLMQGGICRLFFCHSGEKKRDICSDPWNRCVSN	65							
Query Match 60.2%; Score 228; DB 6; Length 82;										
Best Local Similarity 66.7%; Pred. No. 1.4e-23;										
Matches	40;	Conservative	6;	Mismatches	8;	Indels	6;	Gaps	1;	
RESULT 7										
O97942	PRELIMINARY; PRT; 64 AA.									
ID	O97942	PRELIMINARY; PRT; 64 AA.								
AC	O97942;									
DT	01-MAY-1999	(TrEMBLrel. 10, Created)								
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)								
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)								
DE	Beta defensin-2 precursor.									
DE	Capra hircus (Goat).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;									
OC	Bovidae; Caprinae; Capra.									
OX	NCBI_TaxID=9925;									
RN	[1]	SEQUENCE FROM N.A.								
RP	MEDLINE=20002622;	PubMed=10531296;								
RA	Zhao C., Nguyen T., Liu L., Shamova O., Brogden K., Lehrer R.I.;									
RT	"Differential expression of caprine beta-defensins in digestive and respiratory tissues.";									
RL	Infect. Immun. 67:6221-6224(1999).									
RL	EMBL; AJ009877;	CAA08905.1; -								
DR	HSP; P46170;	1ENB.								
DR	GO; GO:0005576;	C:extracellular; IEA.								
DR	GO; GO:0003795;	F:antimicrobial peptide activity; IEA.								
DR	GO; GO:0006932;	P:defense response; IEA.								
DR	InterPro; IPR001855;	Defensin_beta.								
DR	InterPro; IPR006080;	Defensin_mammal.								
DR	Pfam; PF00711;	Defensin_beta; 1.								
DR	SMART; SM00048;	DEFEN; 1.								

Query Match 18.7%; Score 71; DB 6; Length 29;
Best Local Similarity 77.8%; Pred. No. 0.019;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKVLLFAVFLVORNS 18
Db 1 MKVFLFAVFLVORNS 18

RESULT 10
Q80UP9 PRELIMINARY; PRT; 341 AA.

AC Q80UP9; (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE LOC216790 protein (Fragment).
GN LOC216790.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.; and initial analysis of more than 15,000 full-length human
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046431; AAH46431.1; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR01245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00069; Pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT NON TER 1
SQ SEQUENCE 341 AA; 38078 MW; 63BD82E3FFD71914 CRC64;

Query Match 18.2%; Score 69; DB 11; Length 341;
Best Local Similarity 28.8%; Pred. No. 0.45;
Matches 17; Conservative 1; Mismatches 21; Indels 10; Gaps 2;

Qy 18 SGDIP---PGIRNTVCFMQRGHCRLFMCRSGERKG-----DICSDPWNRCVSSSIK 66
Db 235 SGEFSESEGRFDLQKGLRKLRLSRVAGLSGVAFLQSLCAQPNRPFCASTCLQ 293

RESULT 11
Q7YS43 PRELIMINARY; PRT; 64 AA.

AC Q7YS43;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Enteric beta defensin preproprotein.
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP SEQUENCE FROM N.A.
RA Das D.K., Kumar A.;
RT "Cloning and Characterization of Enteric Beta Defensin (EBD) cDNA in
RT Buffalo (Bubalus bubalis).";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY301005; AAP57565.1; -
SQ SEQUENCE 64 AA; 7054 MW; 498B399816C005E CRC64;

Query Match 17.9%; Score 68; DB 6; Length 64;
Best Local Similarity 31.6%; Pred. No. 0.11;
Matches 18; Conservative 7; Mismatches 30; Indels 2; Gaps 2;

Qy 5 LLFAVFLVORNSGDIPPGIRN-TVCFMQRGHCRLFMCRSGERKGDICSDPWNRC 60
Db 6 LLALLFLVLASGSG-FTQGVNPSQCHRNKGICVPIRCPGNMRQIGTCLGPPVKCC 61

RESULT 12
Q95JD2 PRELIMINARY; PRT; 64 AA.

AC Q95JD2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Beta-defensin-3 (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Duit L.A., Langermans J.A.M., Ravensbergen B., Paltansing S.,
RA Vervenne R.A.W., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
RT "Expression of chimpanzee (Pan troglodytes) beta-defensin-3";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY333883; AAK61549.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0003795; F:antimicrobial peptide activity; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
FT NON TER 64
SQ SEQUENCE 64 AA; 7299 MW; 01C90D4B60218DC8 CRC64;

Query Match 17.4%; Score 66; DB 6; Length 64;
Best Local Similarity 31.7%; Pred. No. 0.21;
Matches 19; Conservative 8; Mismatches 27; Indels 6; Gaps 2;

Qy 5 LLFAVFLVORNSGDIPPGIRNTV---CFMQRGHCRLFMCRSGERKGDICSDPWNRC 60
Db 6 LLFALLFLVLPVFGH--GGIINTLQKYCRVGRGRCVLTCLPKPQIGKCKTRGRKCC 63

RESULT 13

Q8LMU8 PRELIMINARY; PRT; 729 AA.

AC Q8LMU8

DT 01-OCT-2002 (T-EMBLrel. 22, Created)

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN OSUNBA0040E17.32.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoidae; Oryzaceae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=cv. Nipponbare;

RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,

RA Overton II L.L., Bera J.J., Tsirir T., Krol M.I., Jarrahi B.B.,

RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,

RA Uterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,

RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.,

RA "Oryza sativa chromosome 10 BAC OSUNBA0040E17 genomic sequence.";

RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RN SEQUENCE FROM N.A.

RP STRAIN=cv. Nipponbare;

RC The Rice Chromosome 10 Sequencing Consortium;

RA "In-depth view of structure, activity, and evolution of rice

RT Chromosome 10.";

RL Science 300:1566-1569(2003).

RN [3]

RN SEQUENCE FROM N.A.

RP STRAIN=cv. Nipponbare;

RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC097278; AAM93469.1; -

DR EMBL; AE017067; AAP52549.1; -

DR Gramene; Q8LMU8; -

DR InterPro; IPR007658; DUF594.

DR Pfam; PF04578; DUF594; 1.

KW Hypothetical protein.

SQ SEQUENCE 729 AA; 82584 MW; 8FFC11FC675783A CRC64;

Query Match 17.4%; Score 66; DB 10; Length 729;

Best Local Similarity 28.8%; Pred. No. 2.5;

Matches 19; Conservative 12; Mismatches 25; Indels 10; Gaps 4;

QY 2 KULLFAVFCLVQRNSGDIIPGIRNTV----CFMORGHCLFMCRSGERKGDICSDP-- 55

DB 489 EVLSNTMFLVVKPNM--LPGAARHNIHLPSCEQIEGHCR--MGFGKXDNFVAASPI 544

QY 56 WNRCCV 61

DB 545 WNPYCM 550

RESULT 14

Q9TU00 PRELIMINARY; PRT; 96 AA.

AC Q9TU00

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Alpha-defensin 1.

GN MNP1.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

OC Cercopitheciinae; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RN SEQUENCE FROM N.A.

RP

RA Zhao C., Nguyen T., Lehrer R.I.;

RT "cDNA cloning of three alpha-defensins and three demidefensins from

RL rhesus monkey bone marrow.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF184159; AAF07925.1; -

DR HSSP; P11479; IDFN.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0003795; F:antimicrobial peptide activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR InterPro; IPR006081; Defensin_alpha.

DR InterPro; IPR006080; Defensin_mammal.

DR InterPro; IPR002366; Defensin_propep.

DR Pfam; PF00323; defensins; 1.

DR Pfam; PF00879; Defensin_propep; 1.

DR SMART; SM00048; DEFSN; 1

DR PROSITE; PS00269; DEFENSIN; 1.

SQ SEQUENCE 96 AA; 10534 MW; A473B80CBFF575A2 CRC64;

Query Match 17.3%; Score 65.5; DB 6; Length 96;

Best Local Similarity 35.6%; Pred. No. 0.38;

Matches 16; Conservative 5; Mismatches 15; Indels 9; Gaps 3;

QY 20 DIPPGIR-NTVCFMQRGHCLFMCRSGERKGDIC---SDPWRCC 60

DB 57 DSVFGLRKNMACY-----CRIPACLAGERRYGTCFYLGRVNAFCC 96

RESULT 15

Q9TTZ9 PRELIMINARY; PRT; 96 AA.

AC Q9TTZ9

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Alpha-defensin 1A.

GN MNP1A.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

OC Cercopitheciinae; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RN SEQUENCE FROM N.A.

RA Zhao C., Nguyen T., Lehrer R.I.;

RT "cDNA cloning of three alpha-defensins and three demidefensins from

RL rhesus monkey bone marrow.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF184160; AAF07926.1; -

DR PIR; A59076; A59076.

DR HSSP; P11479; IDFN.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0003795; F:antimicrobial peptide activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR InterPro; IPR006081; Defensin_alpha.

DR InterPro; IPR006080; Defensin_mammal.

DR InterPro; IPR002366; Defensin_propep.

DR Pfam; PF00323; defensins; 1.

DR Pfam; PF00879; Defensin_propep; 1.

DR SMART; SM00048; DEFSN; 1

DR PROSITE; PS00269; DEFENSIN; 1.

SQ SEQUENCE 96 AA; 10516 MW; A536B80CBFF575A2 CRC64;

Query Match 17.3%; Score 65.5; DB 6; Length 96;

Best Local Similarity 35.6%; Pred. No. 0.38;

Matches 16; Conservative 5; Mismatches 15; Indels 9; Gaps 3;

QY 20 DIPPGIR-NTVCFMQRGHCLFMCRSGERKGDIC---SDPWRCC 60

DB 57 DSVFGLRKNMACY-----CRIPACLAGERRYGTCFYLGRVNAFCC 96

Search completed: June 14, 2004, 16:40:33

Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2004, 16:28:58 ; Search time 56 Seconds
(without alignments)
343.093 Million cell updates/sec

Title: US-10-623-629-2
Perfect score: 379
Sequence: 1 MKVLLFAVFFCLVQRNSGD.....GDICSDPMNRCCVSSSIKNR 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001s.*
 - 5: Geneseq2002s.*
 - 6: Geneseq2003as.*
 - 7: Geneseq2003bs.*
 - 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	379	100.0	68	5 ABB83977	Abb83977 Rat Binlb
2	286	75.5	80	4 AAB84567	Aab84567 Amino aci
3	276	72.8	80	4 AAB84568	Aab84568 Amino aci
4	260	68.6	45	5 ABB83978	Abb83978 Rat Binlb
5	227	59.9	64	4 AAB84579	Aab84579 Amino aci
6	217	57.3	62	4 AAB84588	Aab84588 Amino aci
7	217	57.3	64	4 AAB84580	Aab84580 Amino aci
8	217	57.3	109	4 AAB84577	Aab84577 Amino aci
9	217	57.3	133	4 AAB84565	Aab84565 Amino aci
10	207	54.6	62	4 AAB84589	Aab84589 Amino aci
11	207	54.6	109	4 AAB84578	Aab84578 Amino aci
12	207	54.6	133	4 AAB84566	Aab84566 Amino aci
13	197	52.0	35	6 ABR43520	Abr43520 Mouse bet
14	167	44.1	39	6 ABR43588	Abr43588 Human bet
15	165	43.5	35	6 ABR43519	Abr43519 Human bet
16	144	38.0	31	5 AAM49583	Aam49583 Human bet
17	76.5	20.2	123	4 AAB36670	Aab36670 Human sec
18	76.5	20.2	123	6 ADA56887	Ada56887 Human sec
19	76.5	20.2	123	6 ADA40741	Ada40741 Human sec
20	76.5	20.2	123	6 ABR47725	Abr47725 Human sec
21	76.5	20.2	124	2 AAY36298	Aay36298 Human sec
22	76.5	20.2	124	6 ADA11608	Ada11608 Human nov
23	75	19.8	64	5 AAU91052	Aau91052 Transplan
24	74	19.5	111	4 AAB47331	Aab47331 FCTR8. 8/
25	74	19.5	111	5 AAU83135	Aau83135 Novel sec

26	73	19.3	31	6 ABR43538	Abr43538 Mouse bet
27	72	19.0	50	4 AAB84561	Aab84561 Amino aci
28	72	19.0	64	5 AAU91051	Aau91051 Transplan
29	70.5	18.6	32	6 ABR43553	Abr43553 Mouse bet
30	69	18.2	50	4 AAB84562	Aab84562 Amino aci
31	69	18.2	548	4 AAB30572	Aab30572 A full le
32	68.5	18.1	87	4 AAM78915	Aam78915 Human pro
33	68.5	18.1	87	4 AAB60637	Aab60637 Human NAD
34	68.5	18.1	87	6 ABR58636	Abr58636 Human can
35	68.5	18.1	35	6 AAO22651	Aao22651 Maize bas
36	68.5	18.1	89	6 AAO22650	Aao22650 Maize bas
37	68.5	18.1	92	4 ABB03256	Abb03256 Human mus
38	68.5	18.1	92	6 ABUI2550	Abui2550 Novel hum
39	67	17.7	37	6 ABR43597	Abr43597 Human bet
40	66	17.4	65	2 AAY07243	Aay07243 Beta-defe
41	66	17.4	67	2 AAY07244	Aay07244 Beta-defe
42	66	17.4	67	3 AAB10602	Aab10602 Human SAP
43	66	17.4	67	5 AAU09707	Aau09707 Human bet
44	66	17.4	67	5 AAU91016	Aau91016 Transplan
45	66	17.4	67	5 AAU91036	Aau91036 Transplan

ALIGNMENTS

RESULT 1
ABB83977
ID ABB83977 standard; protein; 68 AA.
XX
AC ABB83977;
XX
DT 09-DEC-2002 (first entry)
XX
DE Rat Binlb SEQ ID NO 2.
XX
KW Rat; Binlb; antibacterial; infection; urinogenital system;
KW sperm maturation.
XX
OS Rattus norvegicus.
XX
FN WO200268463-A1.
XX
PD 06-SEP-2002.
XX
PF 21-JAN-2002; 2002WO-CNO00032.
XX
PR 22-JAN-2001; 2001CN-00105283.
XX
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
XX
PI Zhang Y, Chan H, Li P, He B, So S, Chung Y, Shang Q, Zhang Y;
XX
DR WPI; 2002-682810/73.
XX
N-ESDB; ABV73546, ABV73553, ABV73554.
XX
PT Natural antibacterial Binlb proteins, and encoding polynucleotides,
PT associated with male reproduction especially sperm maturation, applicable
PT in treating disorders like infection of urinogenital system.
XX
PS Example 2; Fig 2A; 35pp; Chinese.
XX
CC The invention relates to an isolated or purified antibacterial Binlb
CC polypeptide. The peptide is for pharmaceutical compositions which are
CC applicable in treating disorders like infections of urinogenital system.
CC The polypeptide and its encoding polynucleotide are associated with male
CC reproduction especially sperm maturation. The present sequence is that of
CC the rat Binlb protein of the invention
XX
SQ Sequence 68 AA;

Query Match 100.0%; Score 379; DB 5; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.2e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLLFAVFFCLVQNSGDI PPGRINTVCFMQRGHCHLFCMCRSGERKGDICSDPWNRC 60
DB 1 MKVLLFAVFFCLVQNSGDI PPGRINTVCFMQRGHCHLFCMCRSGERKGDICSDPWNRC 60
QY 61 VSSSIKQR 68
DB 61 VSSSIKQR 68

RESULT 2
AAB84567
ID AAB84567 standard; protein; 80 AA.
XX
AC AAB84567;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a human EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Homo sapiens.
XX
FN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
DR N-PSDB; AAH28182.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 6; Page 41; 81pp; English.

XX The present sequence represents an antimicrobial peptide expressed in the
XX primate epididymis, designated EP2. The EP2 peptides are comprised of one
XX or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
XX and interact with the membrane of invading pathogens to cause disruptive
XX changes in their permeability. Compositions comprising the EP2 peptides
XX and nucleic acids may be administered to treat microbial infections, to
XX supplement the endogenous production of EP2 peptides for resisting a
XX microbial infection. The EP2 peptides may be used to treat animals
XX (especially those suffering from epithelial infections (e.g.
XX epididymitis), urogenital tract infections and sexually transmitted
XX diseases) and humans and in agricultural and industrial applications.
XX Microorganisms susceptible to EP2 peptides include *Neisseria gonorrhoeae*,
XX *Chlamydia trachomatis*, *Pseudomonas aeruginosa*, *Escherichia coli*,
XX *Staphylococcus aureus*, *Mycobacterium tuberculosis*, *Hemophilus influenzae*,
XX *Streptococcus pneumoniae*, *Brucella abortus*, *Brucella melitensis*,
XX *Aspergillus fumigatus*, *Candida albicans*, *Candida tropicalis*,
XX *Cycomegalovirus*, *ovine lentivirus (OVLV)*, *filaria*, *schistosoma* and/or
XX amebae. The EP2 peptides are especially suitable for use in the
XX production of male and female condoms

XX Sequence 80 AA;

Query Match 75.5%; Score 286; DB 4; Length 80;
Best Local Similarity 75.6%; Pred. No. 9.9e-26;
Matches 49; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKVLLFAVFFCLVQNSGDI PPGRINTVCFMQRGHCHLFCMCRSGERKGDICSDPWNRC 60

DB 1 MKVFFLFAVFLCVQNSGDVPPGIRNTICRMQOGICRLFFCHSGEKKRDICSDPWNRC 60
QY 61 VSSS 64
DB 61 VSNT 64

RESULT 3
AAB84568
ID AAB84568 standard; protein; 80 AA.
XX
AC AAB84568;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a chimpanzee EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Pan troglodytes.
XX
FN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
DR N-PSDB; AAH28183.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 6; Page 41; 81pp; English.

XX The present sequence represents an antimicrobial peptide expressed in the
XX primate epididymis, designated EP2. The EP2 peptides are comprised of one
XX or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
XX and interact with the membrane of invading pathogens to cause disruptive
XX changes in their permeability. Compositions comprising the EP2 peptides
XX and nucleic acids may be administered to treat microbial infections, to
XX supplement the endogenous production of EP2 peptides for resisting a
XX microbial infection. The EP2 peptides may be used to treat animals
XX (especially those suffering from epithelial infections (e.g.
XX epididymitis), urogenital tract infections and sexually transmitted
XX diseases) and humans and in agricultural and industrial applications.
XX Microorganisms susceptible to EP2 peptides include *Neisseria gonorrhoeae*,
XX *Chlamydia trachomatis*, *Pseudomonas aeruginosa*, *Escherichia coli*,
XX *Staphylococcus aureus*, *Mycobacterium tuberculosis*, *Hemophilus influenzae*,
XX *Streptococcus pneumoniae*, *Brucella abortus*, *Brucella melitensis*,
XX *Aspergillus fumigatus*, *Candida albicans*, *Candida tropicalis*,
XX *Cycomegalovirus*, *ovine lentivirus (OVLV)*, *filaria*, *schistosoma* and/or
XX amebae. The EP2 peptides are especially suitable for use in the
XX production of male and female condoms

XX Sequence 80 AA;

Query Match 72.8%; Score 276; DB 4; Length 80;
Best Local Similarity 75.0%; Pred. No. 1.5e-24;
Matches 48; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MKVLLFAVFFCLVQNSGDI PPGRINTVCFMQRGHCHLFCMCRSGERKGDICSDPWNRC 60
DB 1 MKVFFLFAVFLCVQNSGDVPPGIRNTICRMQOGICRLFFCHSGEKKRDICSDPWNRC 60

QY 61 VSSS 64
DB 61 VSNT 64

RESULT 4
ABB83978
ID ABB83978 standard; protein; 45 AA.
AC ABB83978;
XX 09-DEC-2002 (first entry)
DT XX
DE XX
DE Rat Binlb C-terminal region SEQ ID NO 3.
XX Rat; Binlb; antibacterial; infection; urogenital system;
KW sperm maturation.
XX Rattus norvegicus.
OS XX
XX WO200268463-A1.
PN XX
XX 06-SEP-2002.
PD XX
PF 21-JAN-2002; 2002WO-CN0000032.
XX 22-JAN-2001; 2001CN-00105283.
PR XX
XX (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
PA Zhang Y, Chan H, Li P, He B, So S, Chung Y, Shang Q, Zhang Y;
PI WPI; 2002-682810/73.
XX Natural antibacterial Binlb proteins, and encoding polynucleotides,
XX associated with male reproduction especially sperm maturation, applicable
XX in treating disorders like infection of urogenital system.
XX Example 2; Fig 2A; 35pp; Chinese.
XX
XX The invention relates to an isolated or purified antibacterial Binlb
XX polypeptide. The peptide is for pharmaceutical compositions which are
XX applicable in treating disorders like infections of urogenital system.
XX The polypeptide and its encoding polynucleotide are associated with male
XX reproduction especially sperm maturation. The present sequence is that of
XX the C-terminal region of the rat Binlb protein of the invention
SQ Sequence 45 AA;
Query Match 68.6%; Score 260; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.9e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 GIRNTVCFMQRGHCRLFMCSGERKGDICSDPNRCCVSSIXNR 68
DB 1 GIRNTVCFMQRGHCRLFMCSGERKGDICSDPNRCCVSSIXNR 45
RESULT 5
AAB84579
ID AAB84579 standard; protein; 64 AA.
XX AAB84579;
XX 05-SEP-2001 (first entry)
DT XX
DE Amino acid sequence of a mature human EP2 peptide.
XX Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX

OS Homo sapiens.
XX WO200149702-A1.
PN 12-JUL-2001.
PD XX
PF 05-JAN-2001; 2001WO-US0000432.
XX 05-JAN-2000; 2000US-0174513P.
PR (UYEM-) UNIV EMORY.
XX Froelich O, Young LG;
XX WPI; 2001-418353/44.
DR XX
XX Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
PF Claim 3; Page 46; 81pp; English.
XX AAB84571-82 represent mature antimicrobial peptides, expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Apegerillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OVLV), filaria, schistosoma and/or
CC anebae. The EP2 peptides are especially suitable for use in the
XX production of male and female condoms
XX Sequence 64 AA;
SQ
Query Match 59.9%; Score 227; DB 4; Length 64;
Best Local Similarity 77.1%; Pred. No. 6.1e-19;
Matches 37; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 17 NSGDIPGIRNTVCFMQRGHCRLFMCSGERKGDICSDPNRCCVSSS 64
DB 1 NSGDVPPGIRNTVCFMQRGHCRLFMCSGERKGDICSDPNRCCVSSNT 48
RESULT 6
AAB84588
ID AAB84588 standard; peptide; 62 AA.
XX AAB84588;
XX 05-SEP-2001 (first entry)
DT XX
DE Amino acid sequence of an EP2 peptide module.
XX Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX Homo sapiens.
OS WO200149702-A1.
PN 12-JUL-2001.
PD XX
PF 05-JAN-2001; 2001WO-US0000432.
XX

XX 05-JAN-2000; 2000US-0174513P.
XX (UYEM-) UNIV EMORY.
XX Froelich O, Young LG;
XX WPI; 2001-418353/44.
XX Antimicrobial peptides from primate epididymis, useful in the production
XX of condoms for preventing sexually transmitted diseases.
XX Claim 3; Page 49; 81pp; English.
XX AAB84583-89 represent modules of antimicrobial peptides expressed in the
XX primate epididymis, designated EP2. The EP2 peptides are comprised of one
XX or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
XX and interact with the membrane of invading pathogens to cause disruptive
XX changes in their permeability. Compositions comprising the EP2 peptides
XX and nucleic acids may be administered to treat microbial infections, to
XX supplement the endogenous production of EP2 peptides for resisting a
XX microbial infection. The EP2 peptides may be used to treat animals
XX (especially those suffering from epithelial infections (e.g.
XX epididymitis), urogenital tract infections and sexually transmitted
XX diseases) and humans and in agricultural and industrial applications.
XX Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
XX Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
XX Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
XX Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
XX Aspergillus fumigatus, Candida albicans, Candida tropicalis,
XX Cytomegalovirus, ovine lentivirus (OVLV), filaria, schistosoma and/or
XX anebae. The EP2 peptides are especially suitable for use in the
XX production of male and female condoms
XX Sequence 62 AA;

Query Match 57.3%; Score 217; DB 4; Length 62;
Best Local Similarity 76.1%; Pred. No. 8.6e-18;
Matches 35; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 19 GDTPPGIRNTVCFMORGHCRFLMCRSGRKGDCSDPNRCCVSS 64
DB 1 GDVPPGIRNTICRMQOGICRFFCHSGRKGDCSDPNRCCVSSNT 46

RESULT 7
AAB84580
ID AAB84580 standard; protein; 64 AA.
XX AAB84580;
XX 05-SEP-2001 (first entry)
XX Amino acid sequence of a mature chimpanzee EP2 peptide.
XX Antimicrobial peptide; primate epididymis; EP2; microbial infection;
XX epithelial infection; epididymitis; urogenital tract infection;
XX sexually transmitted disease; condom.
XX Pan troglodytes.
XX WO200149702-A1.
XX 12-JUL-2001.
XX 05-JAN-2001; 2001WO-US000432.
XX 05-JAN-2000; 2000US-0174513P.
XX (UYEM-) UNIV EMORY.
XX Froelich O, Young LG;

DR WPI; 2001-418353/44.
XX Antimicrobial peptides from primate epididymis, useful in the production
XX of condoms for preventing sexually transmitted diseases.
XX Claim 3; Page 47; 81pp; English.
XX AAB84571-82 represent mature antimicrobial peptides, expressed in the
XX primate epididymis, designated EP2. The EP2 peptides are comprised of one
XX or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
XX and interact with the membrane of invading pathogens to cause disruptive
XX changes in their permeability. Compositions comprising the EP2 peptides
XX and nucleic acids may be administered to treat microbial infections, to
XX supplement the endogenous production of EP2 peptides for resisting a
XX microbial infection. The EP2 peptides may be used to treat animals
XX (especially those suffering from epithelial infections (e.g.
XX epididymitis), urogenital tract infections and sexually transmitted
XX diseases) and humans and in agricultural and industrial applications.
XX Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
XX Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
XX Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
XX Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
XX Aspergillus fumigatus, Candida albicans, Candida tropicalis,
XX Cytomegalovirus, ovine lentivirus (OVLV), filaria, schistosoma and/or
XX anebae. The EP2 peptides are especially suitable for use in the
XX production of male and female condoms
XX Sequence 64 AA;

Query Match 57.3%; Score 217; DB 4; Length 64;
Best Local Similarity 75.0%; Pred. No. 8.9e-18;
Matches 36; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 17 NSGDIPGIRNTVCFMORGHCRFLMCRSGRKGDCSDPNRCCVSS 64
DB 1 NSGDVPLGIRNTICRMQOGICRFFCHSGRKGDCSDPNRCCVSSNT 48

RESULT 8
AAB84577
ID AAB84577 standard; protein; 109 AA.
XX AAB84577;
XX 05-SEP-2001 (first entry)
XX Amino acid sequence of a mature human EP2 peptide.
XX Antimicrobial peptide; primate epididymis; EP2; microbial infection;
XX epithelial infection; epididymitis; urogenital tract infection;
XX sexually transmitted disease; condom.
XX Homo sapiens.
XX WO200149702-A1.
XX 12-JUL-2001.
XX 05-JAN-2001; 2001WO-US000432.
XX 05-JAN-2000; 2000US-0174513P.
XX (UYEM-) UNIV EMORY.
XX Froelich O, Young LG;
XX WPI; 2001-418353/44.

XX Antimicrobial peptides from primate epididymis, useful in the production
XX of condoms for preventing sexually transmitted diseases.
XX Claim 3; Page 45; 81pp; English.

CC AAB84571-82 represent mature antimicrobial peptides, expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include *Neisseria gonorrhoeae*,
CC *Chlamydia trachomatis*, *Pseudomonas aeruginosa*, *Escherichia coli*,
CC *Staphylococcus aureus*, *Mycobacterium tuberculosis*, *Hemophilus influenzae*,
CC *Streptococcus pneumoniae*, *Brucella abortus*, *Brucella melitensis*,
CC *Aspergillus fumigatus*, *Candida albicans*, *Candida tropicalis*,
CC *Cytomegalovirus*, *ovine lentivirus (OVLV)*, *filaria*, *schistosoma* and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX Sequence 109 AA;

Query Match 57.3%; Score 217; DB 4; Length 109;
Best Local Similarity 76.1%; Pred. No. 1.9e-17;
Matches 35; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 19 GDIPPGIRNTVCFMQRGHCRLFCRSGERKGDICSDPWNRCVSSS 64
DB 48 GDVPPGIRNTICRQQQICRLFFCHSGEKRDICSDPWNRCVSSNT 93

RESULT 9

AAB84565
ID AAB84565 standard; protein; 133 AA.

AC AAB84565;

DT 05-SBP-2001 (first entry)

XX Amino acid sequence of a human EP2 peptide.

XX Antimicrobial peptide; primate epididymis; EP2; microbial infection;
XX epithelial infection; epididymitis; urogenital tract infection;
XX sexually transmitted disease; condom.

OS Homo sapiens.

XX WO200149702-A1.

XX 12-JUL-2001.

XX 05-JAN-2001; 2001WO-US000432.

XX 05-JAN-2000; 2000US-0174513P.

XX (UYEM-) UNIV EMORY.

XX Froelich O, Young LG;

XX WPI; 2001-418353/44.

XX N-PSDB; AAH28180.

XX Antimicrobial peptides from primate epididymis, useful in the production
XX of condoms for preventing sexually transmitted diseases.

PS Claim 6; Page 39-40; 81pp; English.

CC The present sequence represents an antimicrobial peptide expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to

CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include *Neisseria gonorrhoeae*,
CC *Chlamydia trachomatis*, *Pseudomonas aeruginosa*, *Escherichia coli*,
CC *Staphylococcus aureus*, *Mycobacterium tuberculosis*, *Hemophilus influenzae*,
CC *Streptococcus pneumoniae*, *Brucella abortus*, *Brucella melitensis*,
CC *Aspergillus fumigatus*, *Candida albicans*, *Candida tropicalis*,
CC *Cytomegalovirus*, *ovine lentivirus (OVLV)*, *filaria*, *schistosoma* and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX Sequence 133 AA;

Query Match 57.3%; Score 217; DB 4; Length 133;
Best Local Similarity 76.1%; Pred. No. 1.9e-17;
Matches 35; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 19 GDIPPGIRNTVCFMQRGHCRLFCRSGERKGDICSDPWNRCVSSS 64
DB 72 GDVPPGIRNTICRQQQICRLFFCHSGEKRDICSDPWNRCVSSNT 117

RESULT 10

AAB84589
ID AAB84589 standard; peptide; 62 AA.

XX AAB84589;

XX 05-SBP-2001 (first entry)

XX Amino acid sequence of an EP2 peptide module.

XX Antimicrobial peptide; primate epididymis; EP2; microbial infection;
XX epithelial infection; epididymitis; urogenital tract infection;
XX sexually transmitted disease; condom.

OS Pan troglodytes.

XX WO200149702-A1.

XX 12-JUL-2001.

XX 05-JAN-2001; 2001WO-US000432.

XX 05-JAN-2000; 2000US-0174513P.

XX (UYEM-) UNIV EMORY.

XX Froelich O, Young LG;

XX WPI; 2001-418353/44.

XX Antimicrobial peptides from primate epididymis, useful in the production
XX of condoms for preventing sexually transmitted diseases.

PS Claim 3; Page 50; 81pp; English.

CC AAB84583-89 represent modules of antimicrobial peptides expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include *Neisseria gonorrhoeae*,
CC *Chlamydia trachomatis*, *Pseudomonas aeruginosa*, *Escherichia coli*,

in search, using sw model

June 14, 2004, 16:38:04 ; Search time 25 Seconds
(without alignments)

US-10-623-629-2
379
1 MKVLLFAVFFCLVORNSGD.....GDICSDPWNRCVSSSIQNR 68

BLOSUM62
Gapop 10.0 , Gapext 0.5

389414 seqs, 51625971 residues

hits satisfying chosen parameters: 389414

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length: 0
length: 2000000000
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Minimum Match 0%

Listing first 45 summaries

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Issued_Patents_AA: *
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2: /cgn2_6/prodata/2/aa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/aa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/aa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/aa/6CTUG_COMB.pep.*
6: /cgn2_6/prodata/2/aa/backfiles1.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	66	17.4	65	4	US-09-636-399A-2	Sequence 2, Appli	
2	66	17.4	67	4	US-09-636-399A-10	Sequence 10, Appli	
3	65.5	17.3	1665	4	US-09-858-664A-2	Sequence 2, Appli	
4	65.5	17.3	1665	4	US-10-274-978-2	Sequence 2, Appli	
5	63.5	16.8	40	1	US-08-033-873-9	Sequence 9, Appli	
6	63.5	16.8	40	2	US-08-356-832-9	Sequence 9, Appli	
7	63.5	16.8	40	3	US-09-988-705-9	Sequence 9, Appli	
8	63	16.6	3635	4	US-09-845-583A-2	Sequence 2, Appli	
9	62.5	16.5	40	1	US-08-033-873-7	Sequence 7, Appli	
10	62.5	16.5	40	2	US-08-356-832-7	Sequence 7, Appli	
11	62.5	16.5	40	3	US-08-988-705-7	Sequence 7, Appli	
12	62.5	16.5	42	1	US-08-033-873-3	Sequence 3, Appli	
13	62.5	16.5	42	2	US-08-356-832-3	Sequence 3, Appli	
14	62.5	16.5	42	3	US-08-988-705-3	Sequence 3, Appli	
15	62	16.4	64	1	US-08-248-016-4	Sequence 4, Appli	
16	62	16.4	64	1	US-08-451-501-4	Sequence 4, Appli	
17	62	16.4	64	2	US-08-713-455A-5	Sequence 5, Appli	
18	62	16.4	64	4	US-09-228-302-8	Sequence 8, Appli	
19	62	16.4	64	5	PCR-US95-06761-4	Sequence 4, Appli	
20	62	16.4	65	1	US-08-248-016-12	Sequence 12, Appli	
21	62	16.4	65	1	US-08-451-501-12	Sequence 12, Appli	
22	62	16.4	65	5	PCR-US95-06761-12	Sequence 12, Appli	
23	62	16.4	94	4	US-09-486-580A-3	Sequence 3, Appli	
24	60	15.8	64	4	US-09-351-657A-8	Sequence 8, Appli	
25	60	15.8	64	4	US-09-351-657A-8	Sequence 8, Appli	
26	59.5	15.7	408	1	US-09-252-991A-30312	Sequence 30312, A	
27	57.5	15.2	38	1	US-08-033-873-8	Sequence 8, Appli	

ALIGNMENTS

RESULT 1
US-09-636-399A-2
; Sequence 2, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Bairdur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636.399A

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/ CURRENT FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRS
; ORGANISM: Homo sapiens
US-09-636-399A-2

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Query Match 17.4%; Score 66; DB 4; Length 65;
Best Local Similarity 31.7%; Pred. No. 0.39;
Matches 19: Conservative 8; Mismatches 27; Indels 6; Gaps 2

Qy 5 LLFAVFFCLVQRNSGDIIPGIRTV---CFMQRGHCHLFWCSGRKGDICSDPNRCC 60

Db 6 LLFALLFLVVPVGH--GGIINTLQYKVRGGRCAVLSCLPKEEQIGKSTRGRKCC 63

```

RESULT 2
; Sequence 10, Application US/096336399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFEN

```

```

; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-636-399A-10

Query Match      17.4%; Score 66; DB 4; Length 67;
Best Local Similarity 31.7%; Pred. No. 0.4;
Matches 19; Conservative 8; Mismatches 27; Indels 6; Gaps 2;

QY    5 LLFAVFFCLVQRNSGDIPIGRNTV----CFMORGHCRFLFMCRSRGKRGDICSDDPNRCC 60
      ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db     6 LLFALLFLPLVPFGH--GGIINTLQKYCRVRGRCVAVLSCLPFKEIQIGKCSTRGRKCC 63

RESULT 3
US-09-858-664A-2
; Sequence 2, Application US/09858664A
; Patent No. 6482624
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL000927-CIP
; CURRENT APPLICATION NUMBER: US/09/858,664A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1665
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-858-664A-2

Query Match      17.3%; Score 65.5; DB 4; Length 1665;
Best Local Similarity 30.0%; Pred. No. 15;
Matches 15; Conservative 9; Mismatches 19; Indels 7; Gaps 1;

QY    24 GIRNTVCFMORGHCRFLFMCRSRGKG-----DICSDPNRCCVSSSIK 66
      || : ::::| | | : | : | : | : | : | : | : | : | : | :
Db     1568 GARDLQRLGRKLIVRSRYAGLSGGAVAFIRSLTCAQPMWRPCASSCLQ 1617

RESULT 4
US-10-274-978-2
; Sequence 2, Application US/10274978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL000927-CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/274,978
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17

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```

1 GENERAL INFORMATION:
2 APPLICANT: SELSTED, MICHAEL E.
3 APPLICANT: CULLOR, JAMES S.
4 TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
5 TITLE OF INVENTION: NEUTROPHILS
6 NUMBER OF SEQUENCES: 22
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: CAMPBELL AND FLORES
9 STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
10 CITY: SAN DIEGO
11 STATE: CALIFORNIA
12 COUNTRY: USA
13 ZIP: 92122
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/356,832
22 FILING DATE: 12-DEC-1994
23 CLASSIFICATION: 514
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/033,873
27 FILING DATE: 19-MAR-1993
28 ATTORNEY/AGENT INFORMATION:
29 NAME: CAMPBELL, CATHRYN A.
30 REGISTRATION NUMBER: 31,815
31 REFERENCE/DOCKET NUMBER: P-UC 9552
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (619) 535-9001
34 TELEFAX: (619) 535-8949
35 INFORMATION FOR SEQ ID NO: 9:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 40 amino acids
38 TYPE: amino acid
39 TOPOLOGY: linear
40 MOLECULE TYPE: peptide
41
42 US-08-356-832-9
43
44 Query Match 16.8%; Score 63.5; DB 2; Length 40;
45 Best Local Similarity 36.8%; Pred. No. 0.47;
46 Matches 14; Conservative 4; Mismatches 19; Indels 1; Gaps 1;
47
48 QY 24 GRTNTV-CFMQRGHCRLFMCRSGERKGDICSDPWRCC 60
49
50 DB 2 GVNFTCTIRNRCFCVPIRCFGRHRIQTGLGPIKCC 39

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RESULT 7
US-08-988-705-9
; Sequence 9, Application US/08988705
; Patent No. 6211148
; GENERAL INFORMATION:
; APPLICANT: Selseled, Michael E.
; APPLICANT: Cullor, James S.
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
; TITLE OF INVENTION: NEUTROPHILS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,705

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/033,873
FILING DATE: 19930319
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 9552
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-033-873-7

Query Match 16.5%; Score 62.5; DB 1; Length 40;
Best Local Similarity 36.8%; Pred. No. 0.62;
Matches 14; Conservative 4; Mismatches 19; Indels 1; Gaps 1;

QY 24 GIRNTV-CFMORGHCRFLFMCRSGERKGDICSDPNRCC 60
Db 2 GVRNFVTCRINRGFCVPICPGHRRIGTCLGPRKCC 39

RESULT 10
US-08-356-832-7
Sequence 7, Application US/08356832
Patent No. 5821224
GENERAL INFORMATION:
APPLICANT: SELSTED, MICHAEL E.
APPLICANT: CULLOR, JAMES S.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
TITLE OF INVENTION: NEUTROPHILS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,832
FILING DATE: 12-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,873
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UC 9552
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-356-832-7

Query Match 16.5%; Score 62.5; DB 2; Length 40;
Best Local Similarity 36.8%; Pred. No. 0.62;
Matches 14; Conservative 4; Mismatches 19; Indels 1; Gaps 1;

QY 24 GIRNTV-CFMORGHCRFLFMCRSGERKGDICSDPNRCC 60
Db 2 GVRNFVTCRINRGFCVPICPGHRRIGTCLGPRKCC 39

RESULT 11
US-08-988-705-7
Sequence 7, Application US/08988705
Patent No. 6211148
GENERAL INFORMATION:
APPLICANT: SELSTED, MICHAEL E.
APPLICANT: CULLOR, JAMES S.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
TITLE OF INVENTION: NEUTROPHILS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,705
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,873
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,832
FILING DATE: 13-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 2918
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-988-705-7

Query Match 16.5%; Score 62.5; DB 3; Length 40;
Best Local Similarity 36.8%; Pred. No. 0.62;
Matches 14; Conservative 4; Mismatches 19; Indels 1; Gaps 1;

QY 24 GIRNTV-CFMORGHCRFLFMCRSGERKGDICSDPNRCC 60

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,832
FILING DATE: 12-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,873
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 9552
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-356-832-3

Query Match 16.5%; Score 62.5; DB 2; Length 42;
Best Local Similarity 37.5%; Pred.No. 0.65;
Matches 15; Conservative 4; Mismatches 20; Indels 1;

Qy 24 GIRNTV-CFWQRGHCRLFMCGESGERKGDICSDPMNRCCVS 62
Db 2 GVRNHVTNRNGFCVPTRCPGRTRQIGTCFGPRIKCCKRS 41

RESULT 14
US-08-988-705-3
Sequence 3, Application US/08988705
Patent No. 6211148
GENERAL INFORMATION:
APPLICANT: Selsated, Michael E.
APPLICANT: Cullor, James S.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
TITLE OF INVENTION: NEUTROPHILS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
City: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,705
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,873
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,832
FILING DATE: 13-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 2918
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949

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Search completed: June 14, 2004, 16:41:35
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 16:40:40 ; Search time 43 Seconds
(without alignments)
445.520 Million cell updates/sec

Title: US-10-623-629-2

Perfect score: 379
Sequence: 1 MKVLLFAVFFCLVQRNSGD.....GDI CSDPWNRCVSSSIKNR 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	286	75.5	80	12	US-10-381-752-9
3	276	72.8	80	12	US-10-381-752-10
4	260	68.6	45	12	US-10-623-629-3
5	227	59.9	64	12	US-10-381-752-21
6	217	57.3	62	12	US-10-381-752-30
7	217	57.3	64	12	US-10-381-752-22
8	217	57.3	109	12	US-10-381-752-19
9	217	57.3	133	12	US-10-381-752-7
10	207	54.6	62	12	US-10-381-752-31
11	207	54.6	109	12	US-10-381-752-20
12	207	54.6	133	12	US-10-381-752-8
13	197	52.0	35	14	US-10-252-734-25
14	165	43.5	35	14	US-10-252-734-24
15	76.5	20.2	124	12	US-10-372-876-136

16	76.5	20.2	124	14	US-10-097-065-136	Sequence 136, Appl
17	75	19.8	64	9	US-09-917-340-88	Sequence 88, Appl
18	74	19.5	111	9	US-09-893-737-122	Sequence 122, Appl
19	74	19.5	111	9	US-09-746-491-16	Sequence 16, Appl
20	73	19.3	31	14	US-10-252-734-43	Sequence 43, Appl
21	72	19.0	60	12	US-10-381-752-3	Sequence 3, Appl
22	72	19.0	54	9	US-09-917-340-87	Sequence 87, Appl
23	70.5	18.6	32	14	US-10-252-734-58	Sequence 58, Appl
24	69	18.2	50	12	US-10-381-752-4	Sequence 4, Appl
25	69	18.2	548	14	US-10-307-019-9	Sequence 9, Appl
26	68.5	18.1	89	14	US-10-205-072-10	Sequence 10, Appl
27	68.5	18.1	89	14	US-10-205-072-12	Sequence 12, Appl
28	68.5	18.1	92	9	US-09-764-877-1203	Sequence 1203, Ap
29	68.5	18.1	92	15	US-10-242-515-1203	Sequence 1203, Ap
30	66	17.4	65	14	US-10-091-166B-2	Sequence 2, Appl
31	66	17.4	65	14	US-10-272-121-2	Sequence 2, Appl
32	66	17.4	65	14	US-10-409-366-2	Sequence 2, Appl
33	66	17.4	65	14	US-10-409-532-2	Sequence 2, Appl
34	66	17.4	67	9	US-09-917-340-52	Sequence 52, Appl
35	66	17.4	67	9	US-09-917-340-72	Sequence 72, Appl
36	66	17.4	67	9	US-09-872-852-2	Sequence 2, Appl
37	66	17.4	67	14	US-10-091-166B-10	Sequence 10, Appl
38	66	17.4	67	14	US-10-272-121-10	Sequence 10, Appl
39	66	17.4	67	14	US-10-409-366-10	Sequence 10, Appl
40	66	17.4	67	14	US-10-409-532-10	Sequence 10, Appl
41	65.5	17.3	96	9	US-09-917-340-90	Sequence 90, Appl
42	65.5	17.3	390	12	US-10-425-114-37530	Sequence 37530, A
43	65.5	17.3	871	14	US-10-307-019-7	Sequence 7, Appl
44	65.5	17.3	871	16	US-10-311-034-20	Sequence 20, Appl
45	65.5	17.3	1351	14	US-10-307-019-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-10-623-629-2

; Sequence 2, Application US/10623629

; Publication No. US20040058371A1

; GENERAL INFORMATION: INSTITUTE OF BIOCHEMISTRY, CHINESE ACADEMY OF SCIENCES

; APPLICANT: SHANGHAI INSTITUTE OF BIOCHEMISTRY, CHINESE ACADEMY OF SCIENCES

; TITLE OF INVENTION: A NOVEL NATURAL ANTIBACTERIAL PEPTIDE, THE NUCLEOTIDE SEQUENCE EN

; TITLE OF INVENTION: IT AND THE

; TITLE OF INVENTION: USE THEREOF

; FILE REFERENCE: 010207 PCWO

; CURRENT APPLICATION NUMBER: US/10/623,629

; CURRENT FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: CN 01105283.X

; PRIOR FILING DATE: 2001-01-22

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 2

; SOFTWARE: Patentin version 3.0

; LENGTH: 68

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-623-629-2

Query Match 100.0%; Score 379; DB 12; Length 68;

Best Local Similarity 100.0%; Pred. No. 5.8e-38; Indels 0; Gaps 0;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKVLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRC 60

Qy 61 VSSSIKNR 68

Db 61 VSSSIKNR 68

RESULT 2

US-10-381-752-9

; Sequence 9, Application US/10381752

Publication No. US20040072777A1
GENERAL INFORMATION:
APPLICANT: SHANGHAI INSTITUTE OF BIOCHEMISTRY, CHINESE ACADEMY OF SCIENCES
TITLE OF INVENTION: A NOVEL NATURAL ANTIBACTERIAL PEPTIDE, THE NUCLEOTIDE SEQUENCE EN
APPLICANT: Froehlich, Otto
TITLE OF INVENTION: IT AND THE
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: 010207 PCWO US/10/623,629
CURRENT APPLICATION NUMBER: US/10/381,752
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: CN 01105283.X
PRIOR FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 45
TYPE: PRT
ORGANISM: Homo sapiens
US-10-623-629-3

Query Match 68.6%; Score 260; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.4e-24; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GIRNTVCFMQRGCHRLFCMCRSGRKGDIKRDICSDPWNRCVSSSIKNR 68
DB 1 GIRNTVCFMQRGCHRLFCMCRSGRKGDIKRDICSDPWNRCVSSSIKNR 45

RESULT 5
US-10-381-752-21
Sequence 21, Application US/10381752
Publication No. US20040072777A1
GENERAL INFORMATION:
APPLICANT: Froehlich, Otto
APPLICANT: Young, Leona G.
TITLE OF INVENTION: Epitidymal Antimicrobial Peptides
FILE REFERENCE: 05501-0132US 43150-251426
CURRENT APPLICATION NUMBER: US/10/381,752
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: PCT/US01/00432
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,513
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 64
TYPE: PRT
ORGANISM: Homo sapiens
US-10-381-752-21

Query Match 59.9%; Score 227; DB 12; Length 64;
Best Local Similarity 77.1%; Pred. No. 9.7e-20;
Matches 37; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 17 NSGDIPFGIRNTVCFMQRGCHRLFCMCRSGRKGDIKRDICSDPWNRCVSSS 64
DB 1 NSGDVPPGIRNTICRMQQGICRLFFCHSGRKGDIKRDICSDPWNRCVSSNT 48

RESULT 6
US-10-381-752-30
Sequence 30, Application US/10381752
Publication No. US20040072777A1
GENERAL INFORMATION:
APPLICANT: Froehlich, Otto
APPLICANT: Young, Leona G.
TITLE OF INVENTION: Epitidymal Antimicrobial Peptides
FILE REFERENCE: 05501-0132US 43150-251426
CURRENT APPLICATION NUMBER: US/10/381,752
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: PCT/US01/00432
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,513

Publication No. US20040072777A1
GENERAL INFORMATION:
APPLICANT: Froehlich, Otto
APPLICANT: Young, Leona G.
TITLE OF INVENTION: Epitidymal Antimicrobial Peptides
FILE REFERENCE: 05501-0132US 43150-251426
CURRENT APPLICATION NUMBER: US/10/381,752
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: PCT/US01/00432
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,513
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 80
TYPE: PRT
ORGANISM: Homo sapiens
US-10-381-752-9

Query Match 75.5%; Score 286; DB 12; Length 80;
Best Local Similarity 76.6%; Pred. No. 1e-26; Indels 9; Gaps 0;
Matches 49; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKVLLFAVFFCLVQRNSGDIPIGIRNTVCFMQRGCHRLFCMCRSGRKGDIKRDICSDPWNRC 60
DB 1 MKVFFLFAVLFCLVQTNSGDIPIGIRNTICRMQQGICRLFFCHSGRKGDIKRDICSDPWNRC 60

QY 61 VSSS 64
DB 61 VSNT 64

RESULT 3
US-10-381-752-10
Sequence 10, Application US/10381752
Publication No. US20040072777A1
GENERAL INFORMATION:
APPLICANT: Froehlich, Otto
APPLICANT: Young, Leona G.
TITLE OF INVENTION: Epitidymal Antimicrobial Peptides
FILE REFERENCE: 05501-0132US 43150-251426
CURRENT APPLICATION NUMBER: US/10/381,752
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: PCT/US01/00432
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,513
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 80
TYPE: PRT
ORGANISM: Pan troglodytes
US-10-381-752-10

Query Match 72.8%; Score 276; DB 12; Length 80;
Best Local Similarity 75.0%; Pred. No. 1.6e-25; Indels 10; Gaps 0;
Matches 48; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

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DB 1 MKVFFLFAVLFCLVQTNSGDIPIGIRNTICRMQQGICRLFFCHSGRKGDIKRDICSDPWNRC 60

QY 61 VSSS 64
DB 61 VSNT 64

RESULT 4
US-10-623-629-3
Sequence 3, Application US/10623629
Publication No. US20040058371A1

; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-381-752-30

Query Match 57.3%; Score 217; DB 12; Length 62;
Best Local Similarity 76.1%; Pred. No. 1.5e-18;
Matches 35; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCVSSS 64
Db 1 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCVSVNT 46

RESULT 7

US-10-381-752-22
; Sequence 22, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
; APPLICANT: Froehlich, Otto
; TITLE OF INVENTION: Epitidymal Antimicrobial Peptides
; FILE REFERENCE: 05501-0132US 43150-251426
; CURRENT APPLICATION NUMBER: US/10/381,752
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/US01/00432
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,513
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-10-381-752-22

Query Match 57.3%; Score 217; DB 12; Length 64;
Best Local Similarity 75.0%; Pred. No. 1.5e-18;
Matches 36; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 17 NSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCVSSS 64
Db 1 NSGDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCVSVNT 48

RESULT 8

US-10-381-752-19
; Sequence 19, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
; APPLICANT: Froehlich, Otto
; TITLE OF INVENTION: Epitidymal Antimicrobial Peptides
; FILE REFERENCE: 05501-0132US 43150-251426
; CURRENT APPLICATION NUMBER: US/10/381,752
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/US01/00432
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,513
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-381-752-19

Query Match 57.3%; Score 217; DB 12; Length 109;
Best Local Similarity 76.1%; Pred. No. 2.6e-18;
Matches 35; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCVSSS 64
Db 48 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCVSVNT 93

RESULT 9

US-10-381-752-7
; Sequence 7, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
; APPLICANT: Froehlich, Otto
; APPLICANT: Young, Leona G.
; TITLE OF INVENTION: Epitidymal Antimicrobial Peptides
; FILE REFERENCE: 05501-0132US 43150-251426
; CURRENT APPLICATION NUMBER: US/10/381,752
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/US01/00432
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,513
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-381-752-7

Query Match 57.3%; Score 217; DB 12; Length 133;
Best Local Similarity 76.1%; Pred. No. 3.2e-18;
Matches 35; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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Db 72 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCVSVNT 117

RESULT 10

US-10-381-752-31
; Sequence 31, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
; APPLICANT: Froehlich, Otto
; APPLICANT: Young, Leona G.
; TITLE OF INVENTION: Epitidymal Antimicrobial Peptides
; FILE REFERENCE: 05501-0132US 43150-251426
; CURRENT APPLICATION NUMBER: US/10/381,752
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/US01/00432
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,513
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-10-381-752-31

Query Match 54.6%; Score 207; DB 12; Length 62;
Best Local Similarity 73.9%; Pred. No. 2.4e-17;
Matches 34; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCVSSS 64
Db 1 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCVSVNT 46

Search completed: June 14, 2004, 16:46:23
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 16:36:35 ; Search time 21 Seconds
(without alignments)
311.477 Million cell updates/sec

Title: US-10-623-629-2
Perfect score: 379
Sequence: 1 MKVLLFAVFFCLVQRNSGD.....GDICSDPWRCCVSSSIKMR 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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PIR 78:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	63.5	16.8	40	2 I45495	beta-defensin-9 -
4	63	16.6	139	2 T34238	hypothetical prote
5	63	16.6	3635	2 T10053	laminin alpha 5 ch
6	62.5	16.5	40	2 G45495	beta-defensin-7 -
7	62.5	16.5	42	2 C45495	beta-defensin-3 -
8	62.5	16.5	118	2 I51574	gene wnt-6 protein
9	62.5	16.5	345	2 T25138	hypothetical prote
10	62.5	16.5	358	2 T25137	hypothetical prote
11	62	16.4	64	2 A56128	lingual antimicrob
12	62	16.4	139	2 T33138	hypothetical prote
13	62	16.4	205	2 H69889	hypothetical prote
14	60.5	16.0	34	2 F34870	cryptidin-4 mouse
15	60.5	16.0	364	2 F34870	wnt-6 protein - mo
16	60.5	16.0	365	2 T34870	soluble-type glyco
17	60	15.8	575	1 VCLJHD	env polyprotein pr
18	59.5	15.7	65	2 A35947	crotonamine 1 precu
19	59.5	15.7	378	2 B59180	wnt inhibitory fac
20	59.5	15.7	555	2 A33723	Cypridina-luciferi
21	59	15.6	644	2 C30585	hypothetical prote
22	58	15.3	101	2 JQ0877	cyc02 protein prec
23	57.5	15.2	41	2 D45495	beta-defensin-4 -
24	57.5	15.2	94	1 A40499	defensin alpha-1 p
25	57.5	15.2	494	2 S97539	probable membrane
26	57.5	15.2	2471	2 A49128	cell-fate determin
27	57	15.0	139	2 T33137	hypothetical prote
28	57	15.0	2555	2 A40043	notch protein homo
29	56.5	14.9	116	2 T10084	lipid transfer pro

ALIGNMENTS

RESULT 1

C35947
crotonamine 3 precursor - tropical rattlesnake
C;Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1993
C;Accession: C35947
R;Smith, L.A.; Schmidt, J.J.
Toxicon 28, 575-585, 1990
A;Title: Cloning and nucleotide sequences of crotonamine genes.
A;Reference number: A35947; MUID:90357261; PMID:2389256
A;Accession: C35947
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-65 <SMI>
C;Superfamily: crotonamine

Query Match 17.8% Score 67.5; DB 2; Length 65;
Best Local Similarity 34.6%; Pred. No. 0.64; 23; Indels 25; Gaps 6;

Matches 27; Conservative 3; Mismatches 3; Indels 25; Gaps 6;

Qy 1 MKVL-LFAVFFCLVQRNSGDIPPIGRNTVCFQVGRHCLFMCRSGRKGIDIC----SD- 54
Db 1 MKILYLLFAFLFLAFLSE-----PGNAYKCHIKGGHC-----PPKGIKICPPSSDF 47

RESULT 2

T08773
hypothetical protein DKFZp586N041.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08773
R;Ottewill, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08773
A;Molecule type: mRNA
A;Residues: 1-276 <OTT>
A;Cross-references: EMBL:AL050140
A;Experimental source: adult uterus; clone DKFZp586N041
C;Genetics:
A;Note: DKFZp586N041.1

Query Match 17.0% Score 64.5; DB 2; Length 276;
Best Local Similarity 29.5%; Pred. No. 4.8; 24; Indels 13; Gaps 2;

Matches 18; Conservative 6; Mismatches 24; Indels 13; Gaps 2;

Qy 8 AVFFCL-----VQNSGDIPPIGRNTVCFQVGRHCLFMCRSGRKGIDICSDPW 56
Db 8 AVFFCL-----VQNSGDIPPIGRNTVCFQVGRHCLFMCRSGRKGIDICSDPW 56

Db 179 ATFYCISQMFREWFVKQKGGDPPGPDNTKIAVTK--CGNVMLRQAGDSGOISSEHW 236

Qy 57 N 57

Db 237 N 237

RESULT 3

I45495
beta-defensin-9 - bovine
N/Alternate names: peptide BNB-9
N/Contains: beta-defensin-8
C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 22-Apr-1995
C/Accession: I45495; H45495
R/Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A/Title: Purification, primary structures, and antibacterial activities of beta-defensin
A/Reference number: A45495; MUID:93203264; PMID:8454635
A/Accession: I45495
A/Molecule type: protein
A/Residues: 1-40 <SEL>
A/Note: sequence modified after extraction from NCBI backbone
A/Accession: H45495
A/Molecule type: protein
A/Residues: 3-40 <SE2>
A/Note: sequence extracted from NCBI backbone (NCBIP:127958)
C/Keywords: pyroglutamic acid
F/1-40/Product: beta-defensin-9 #status experimental <MAL>
F/3-40/Product: beta-defensin-8 #status experimental <MA2>
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 16.8%; Score 63.5; DB 2; Length 40;

Best Local Similarity 36.8%; Pred. No. 1.2; Indels 1; Gaps 1;

Matches 14; Conservative 4; Mismatches 19; Indels 1; Gaps 1;

Qy 24 GIRNTV-CFMQGHGRLFCMCRSGERKGDICSDPNRCC 60

Db 2 GVRNFTCRINRGFCVPIRCPGHRQIGTCLGPRIKCC 39

RESULT 4

T34238
hypothetical protein F22A3.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
C/Accession: T34238
R/Halleworth, K.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid F22A3.
A/Reference number: Z21492
A/Accession: T34238
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-139 <HAL>
A/Cross-references: EMBL:U41547; PIDN:AAA83197.1; CESP:F22A3.6
C/Genetics:
A/Gene: CESP:F22A3.6
A/Introns: 12/1; 49/3; 88/3; 107/3
C/Superfamily: Caenorhabditis elegans hypothetical protein F22A3.6

Query Match 16.6%; Score 63; DB 2; Length 139;

Best Local Similarity 23.9%; Pred. No. 4;

Matches 22; Conservative 12; Mismatches 28; Indels 30; Gaps 5;

Qy 1 MKVLLPFAV-----FCLVORNSGDIPPGIRNTVCFMQRG--HCRLFMCESG-----45

Db 3 VKSLLSVAIYAVVSADCLHCINRGSGCKPIG-----CHMDVGLSCGYIQIKIGYED 57

Qy 46 -----ERKGDICSDPNRCC-----CVSSSIKN 67

Db 58 CGOPTKAGTTEAAWKECADLNCATTCVEN 89

RESULT 5

T10053
laminin alpha 5 chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2003
C/Accession: T10053
R/Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997
A/Reference number: Z16923
A/Accession: T10053
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3635 <MIN>
A/Cross-references: EMBL:U37501; NID:92599231; PID:92599232
C/Genetics:
A/Gene: Lamas
C/Keywords: basement membrane; cell binding; extracellular matrix
F/1688-1939/Domain: laminin-type EGF-like homology <LEG>
F/1942-1970/Domain: EGF homology <EGF>

Query Match 16.6%; Score 63; DB 2; Length 3635;

Best Local Similarity 43.3%; Pred. No. 64;

Matches 13; Conservative 6; Mismatches 7; Indels 4; Gaps 2;

Qy 23 PGIRNTVCFMQGHGRLFCMCRSGERKGDIC 52

Db 469 PGVANSLCDPESGCC---MCRIG-FEGDRC 494

RESULT 6

G45495
beta-defensin-7 - bovine
N/Alternate names: peptide BNB-7
C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C/Accession: G45495
R/Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A/Title: Purification, primary structures, and antibacterial activities of beta-defensin
A/Reference number: A45495; MUID:93203264; PMID:8454635
A/Accession: G45495
A/Molecule type: protein
A/Residues: 1-40 <SEL>
A/Note: sequence modified after extraction from NCBI backbone
C/Keywords: antibacterial; disulfide bond; pyroglutamic acid
F/1-40/Product: beta-defensin-7 #status experimental <MAL>
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 16.5%; Score 62.5; DB 2; Length 40;

Best Local Similarity 36.8%; Pred. No. 1.6;

Matches 14; Conservative 4; Mismatches 19; Indels 1; Gaps 1;

Qy 24 GIRNTV-CFMQGHGRLFCMCRSGERKGDICSDPNRCC 60

Db 2 GVRNFTCRINRGFCVPIRCPGHRQIGTCLGPRIKCC 39

RESULT 7

C45495
beta-defensin-3 - bovine
N/Alternate names: peptide BNB-3
N/Contains: beta-defensin-2
C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C/Accession: C45495; B45495
R/Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A/Title: Purification, primary structures, and antibacterial activities of beta-defensin
A/Reference number: A45495; MUID:93203264; PMID:8454635
A/Accession: C45495

FOR THE

Matches 24; Conservative 9; Mismatches 25; Indels 29; Gaps 5

QY 1 MKVLLP-AVFFCLVNRS------GDIPPG---IRNTVCFMORGHCRLF 40
:::|::|:
Db 79 MRLLLLFLAVFLCRVTAHQDAETCSDDTCCKLGDNLTWGCMPNNAVCCDRSHC --- 135
:::|::|:
QY 41 MCRRGKERKDICSDPNNRCVVSSSIKN 67
:|:|:|:
Db 136 -CFGTG----TTCDPQGARCIGADEKH 156
:|:|:|:

RESULT 10

T25137

Hypothetical protein T22H2.6a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Dec-2002
C:Accession: T25137
R:Lennard, N.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19985
A:Accession: T25137
A>Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-358 <MIL>
A:Cross-references: EMBL:Z81595; PIDN:CAB54304.1; GSDB:GN00019; CESP:T22H2.6a
A:Experimental source: clone T22H2
C:Genetics:
A:Gene: CESP:T22H2.6a
A:Map position: 1
A:Introns: 93/3, 232/3, 314/3
C:Superfamily: protein T22H2.6

Query Match 16.5%; Score 62.5; DB 2; Length 358;
Best Local Similarity 27.6%; Pred. No. 10;
Matches 24; Conservative 9; Mismatches 25; Indels 29; Gaps 5;

QY 1 MKVLLP-AVFFCLVNRS------GDIPPG---IRNTVCFMORGHCRLF 40
:::|::|:
Db 79 MRLLLLFLAVFLCRVTAHQDAETCSDDTCCKLGDNLTWGCMPNNAVCCDRSHC --- 135
:::|::|:
QY 41 MCRRGKERKDICSDPNNRCVVSSSIKN 67
:|:~::~|:
Db 136 -CFGTG----TTCDPQGARCIGADEKH 156
:|:~::~|:

RESULT 11

A56128

Lingual antimicrobial peptide precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Nov-1999
C:Accession: A56128; B56128
R:Schoenwetter, B.S.; Stolsenberg, E.D.; Zaaloff, M.A.
Science 267, 1645-1648, 1995
A>Title: Epithelial antibiotics induced at sites of inflammation.
A:Reference number: A56128; MUID:95192714; PMID:7886453
A:Accession: A56128
A:Molecule type: mRNA
A:Residues: 1-64 <SCH>
A:Cross-references: GB:S76279; NID:g894208; PIDN:AAB33727.1; PID:g894209
A:Accession: B56128
A:Molecule type: protein
A:Residues: 23-64 <SC2>
C:Keywords: antibacterial; antifungal
F:1-20/Domain: signal sequence #status predicted <SIG>
F:23-64/Product: lingual antimicrobial peptide #status experimental <MAT>

Query Match 16.4%; Score 62; DB 2; Length 64;
Best Local Similarity 29.8%; Pred. No. 2.7;
Matches 17; Conservative 8; Mismatches 30; Indels 2; Gaps 2;

QY 5 LLAPVFECIVQRNSGPDIPIGRNT-VCFMORGHCRLFMCRRSGERKGDISDPPNRCC 60
||::|:|:
Db 6 LLLALLFLVLVSAGS-GTGVNRNSQCRRNKGLCVIRCPGSNRQICTLGAQVKCC 61
||::|:|:

QY 1 MKVLLFAVFF-CLVQNSGDIPPGIRNTVCFMQRGHCRLFMCRGSRKGDICSDPWR 58
Db 47 VMLLKLGVPFRFFSBERGKDIPFTQNRCLKLSQHTGI-----ENNR 90

RESULT 14

I48887
cryptdin-4 - mouse (fragment)
N;Alternate names: crypt defensin 4
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 16-Jul-1999
C;Accession: I48887; D43279
R;Huttner, K.M.; Seistad, M.E.; Ouellette, A.J.
Genomics 19, 448-453, 1994
A;Title: Structure and diversity of the murine cryptdin gene family.
A;Reference number: A50017; MUID:94245232; PMID:8188287
A;Accession: I48887
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-34 <RES>
A;Cross-references: EMBL:U03032; NID:9437245; PIDN:AAA57172.1; PID:9437246
R;Selssted, M.E.; Miller, S.I.; Henschen, A.H.; Ouellette, A.J.
J. Cell Biol. 119, 929-936, 1992
A;Title: Enteric defensins: antibiotic peptide components of intestinal host defense.
A;Reference number: A43279; MUID:92363933; PMID:1500431
A;Accession: D43279
A;Molecule type: protein
A;Residues: 3-33 <SEL>
A;Experimental source: intestinal epithelium
A;Note: sequence extracted from NCBI backbone (NCBIP:110696)
C;Genetics:
A;Gene: Defc4
C;Superfamily: mammalian defensin

Query Match 16.0%; Score 60.5; DB 2; Length 34;
Best Local Similarity 30.6%; Pred. No. 2.4;
Matches 11; Conservative 7; Mismatches 13; Indels 5; Gaps 1;

QY 25 IRNTVCFMQRGHCRLFMCRGSRKGDICSDPWRCC 60
Db 1 LRGLCYCRKGH-----CKRGRVRGTCGIRFLYCC 31

RESULT 15

F36470
Wnt-6 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 16-Jul-1999
C;Accession: F36470
R;Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A;Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult
A;Reference number: A36470; MUID:91122634; PMID:2279700
A;Accession: F36470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-364 <GAV>
A;Cross-references: GB:W89800; NID:G202407; PIDN:AAA40569.1; PID:G202408
C;Superfamily: int-1 transforming protein

Query Match 16.0%; Score 60.5; DB 2; Length 364;
Best Local Similarity 30.0%; Pred. No. 18;
Matches 21; Conservative 4; Mismatches 28; Indels 17; Gaps 5;
QY 5 LLFAV---FFCLVQNSGDIPPGIRNTVCFMQR---GHCRLFMCRGSRKGDICSDPWR 51
Db 283 LLYAADSPDFCAPNRTGS--PGTRGRACNSAPPDLSCGDLCCGRHQESVQLENC 340
QY 52 CSDFWNRCCV 61
Db 341 CRFHW--CCV 348

RESULT 12

T33138
hypothetical protein C45G7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C;Accession: T33138
R;Pante, M.; Wamsley, P.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C45G7.
A;Reference number: Z21288
A;Accession: T33138
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-139 <DAN>
A;Cross-references: EMBL:AF067611; PIDN:AAC19181.1; GSPDB:GN00022; CESP:C45G7.2
A;Experimental source: strain Bristol N2; clone C45G7
C;Genetics:
A;Gene: CESP.C45G7.2
A;Map position: 4
A;Introns: 12/1; 49/3; 88/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F22A3.6

Query Match 16.4%; Score 62; DB 2; Length 139;
Best Local Similarity 21.8%; Pred. No. 5.2;
Matches 19; Conservative 18; Mismatches 30; Indels 20; Gaps 4;

QY 1 MKVLLFAV-----FFCLVQNSGDIPPGIRNTVCFMQRGHCRLFM-----C-RSG 45
Db 3 VKAILLSIAVAYASADCLHCICNRESGCKPIGCHMDVGLSCGYQIKIPYYEDCGQP 62

QY 46 ERKGDICSDPWR-----CVSSSIKN 67
Db 63 KKHGSTEVAWKRCADLKLKATNCVEN 89

RESULT 13

H69889
hypothetical protein yndH - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: H69889
R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69889
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-205 <KUN>
A;Cross-references: GB:Z99113; GB:AL009126; NID:G2634090; PIDN:CAB13663.1; PID:G2634163
A;Experimental source: strain 168
C;Genetics:
A;Gene: yndH
C;Superfamily: Bacillus subtilis hypothetical protein yndH

Query Match 16.4%; Score 62; DB 2; Length 205;
Best Local Similarity 27.1%; Pred. No. 7.3;
Matches 16; Conservative 7; Mismatches 20; Indels 16; Gaps 2;

1ue Jun 13 09:03:33 2004

Search completed: June 14, 2004, 16:41:13
Job time : 37 secs

UB-10-023-023-2.1P1

1390

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2004, 16:29:44 ; Search time 14 Seconds
(without alignments)
252.912 Million cell updates/sec

Title: US-10-623-629-2

Perfect score: 379

Sequence: 1 MKVLLFAVFCFLVQRNSG.....GDICDPWNRCCVSSSIKNR 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	76.5	20.2	123	D118_HUMAN	Q96ph6 homo sapien
2	75	19.8	63	BD04_BOVIN	P46162 bos taurus
3	74	19.5	88	D120_HUMAN	Q9n689 homo sapien
4	72	19.0	64	BD01_CAPHI	Q97946 capra hircu
5	71.5	18.9	123	D118_MACMU	Q95110 macaca mula
6	71	18.7	55	BD09_BOVIN	P46167 bos taurus
7	71	18.7	57	BD03_BOVIN	P46161 bos taurus
8	70	18.5	129	WNT6_XENLA	P31287 xenopus lae
9	69	18.2	64	BD01_SHEEP	O39038 ovis aries
10	68.5	18.1	87	NUOS_HUMAN	Q9nrx3 homo sapien
11	67.5	17.8	65	MYX3_CRODU	P24333 crotalus du
12	66	17.4	64	D103_PANTR	Q95jd2 pan troglod
13	66	17.4	64	EAP_BOVIN	O02775 bos taurus
14	66	17.4	67	D103_HUMAN	P81534 homo sapien
15	65.5	17.3	96	DEF1_MACMU	P20030 macaca mula
16	65	17.2	64	BD02_SHEEP	O39039 ovis aries
17	64.5	17.0	96	DEF3_MACMU	P60031 macaca mula
18	64.5	17.0	96	DEF8_MACMU	P60032 macaca mula
19	64.5	17.0	942	D133_HUMAN	Q8tey7 homo sapien
20	63	16.6	3718	LMAS_MOUSE	Q1001 mus musculu
21	62.5	16.5	40	BD07_BOVIN	P46165 bos taurus
22	62.5	16.5	70	D131_HUMAN	P39861 homo sapien
23	62.5	16.5	117	WNT6_PLEDO	P28137 plethodon j
24	62	16.4	64	LAP_BOVIN	Q28880 bos taurus
25	60.5	16.0	92	DEF4_MOUSE	P28311 mus musculu
26	60.5	16.0	364	WNT6_MOUSE	P23727 mus musculu
27	60.5	16.0	365	WNT6_HUMAN	Q3y6f9 homo sapien
28	60	15.8	64	AMP2_MELGA	P00392 meleagris g
29	60	15.8	64	GLI3_CHICK	P46158 gallus gall
30	60	15.8	575	ENV_SMRV	P21412 squirrel mo
31	59.5	15.7	65	MYX1_CRODU	P24331 crotalus du
32	59.5	15.7	378	WTF1_BRARE	Q9w6f9 brachydanio
33	59.5	15.7	555	LUCI_VARHI	P17554 vargula hil

ALIGNMENTS

RESULT 1

ID	D118_HUMAN	STANDARD;	PRT;	123 AA.
AC	Q96PH6; Q9N691; Q9NUH0;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	Beta-defensin 118 precursor (beta-defensin 18) (DEFB-18) (Epididymal secretory protein 13.6) (ESP13.6).			
GN	DEFB118 OR DEFB18 OR ESC42 OR C20ORF63.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Epididymis;			
RC	MEDLINE=21448442; PubMed=11564719;			
RA	Liu Q., Hamil K.G., Sivashanmugam P., Grossman G., Soundararajan R., Rao A.J., Richardson R.T., Zhang Y.-L., O'Rand M.G., Petrusz P., French F.S., Hall S.H.;			
RA	"Primate epididymis-specific proteins: characterization of ESC42, a novel protein containing a trefoil-like motif in monkey and human.";			
RT	Endocrinology 142:4529-4539(2001).			
RL	(2)			
RN	SEQUENCE FROM N.A., AND TISSUE DISTRIBUTION.			
RP	MEDLINE=2705149; PubMed=12600824;			
RA	Kao C.Y., Chen Y., Zhao Y.H., Wu R.;			
RA	"ORFeome-based search of airway epithelial cell-specific novel human beta-defensin genes.";			
RT	Am. J. Respir. Cell Mol. Biol. 29:71-80(2003).			
RL	(3)			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Leharval M.H., Leversha M.A., Lloyd C.M., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,			

Q90y57 brachydanio
P25923 catharanthu
P46166 bos taurus
P59665 homo sapien
P78504 homo sapien
Q9gw30 rattus norv
P46531 homo sapien
P46160 bos taurus
P10975 ricinus com
P28145 thunnus thy
Q9gf3 bungarus ca
P77409 escherichia

RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.M., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RA "The DNA sequence and comparative analysis of human chromosome 20."
 RL Nature 414:865-871 (2001).
 [4]
 RP SEQUENCE OF 23-123 FROM N.A., AND IDENTIFICATION.
 RP TISSUE=B-cell, Fetal lung, and Testis;
 RX MEDLINE=21843921; PubMed=11854508;
 RA Schutte B.C., Mitros J.P., Barlett J.B., Walters J.D., Jia H.P.,
 RA Welsh M.J., Casavant T.L., McCray P.B. Jr.,
 RA "Discovery of five conserved beta-defensin gene clusters using a
 RT computational search strategy."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:2129-2133 (2002).
 CC -1- FUNCTION: Has antibacterial activity (Potential).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: High-level and epididymis-specific expression.
 CC -1- Most abundant in the epithelium of the caput and is also present
 CC in the lumen and bound to sperm. Expressed also in pancreas.
 CC -1- SIMILARITY: Belongs to the beta-defensin family.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC
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 CC
 CC EMBL; AF347073; AAL29987.1; -;
 CC EMBL; AF529415; AAQ09524.1; -;
 CC EMBL; AL031650; CAB72350.2; ALT_SEQ.
 CC EMBL; AY122471; AAM93913.1; -;
 CC Genew; HGNC:16196; DEFB118.
 CC MIM; 607650; -;
 CC GO; GO:0005653; C:perinuclear space; NAS
 CC GO; GO:0003797; F:antibacterial peptide activity; TAS.
 CC GO; GO:0007160; P:cell-matrix adhesion; NAS.
 CC GO; GO:0045087; P:innate immune response; TAS.
 CC GO; GO:0007283; P:spermatogenesis; NAS.
 CC Antibiotic; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 62 BETA-DEFENSIN 118.
 FT PROPEP 65 123 POTENTIAL.
 FT DISULFID 27 54 BY SIMILARITY.
 FT DISULFID 34 48 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 SQ SEQUENCE 123 AA; 13613 MW; 0CBAFDB0A5459BA6 CRC64;
 Query Match 20.2%; Score 76.5; DB 1; Length 123;
 Best Local Similarity 32.4%; Pred. No. 0.023;
 Matches 22; Conservative 10; Mismatches 31; Indels 5; Gaps 3;
 QY 1 MKVLLFAVFFCLVQNSGDIIPGINTVCFMORGHCLFMCRSGRKGDICSDPWRCC 60
 Db 1 MKLLLLALPMLVLLPQ---VIFAYSGEKKCMNRSGHCRK-OCKDGEAVKDTCKN-LRACC 55
 QY 61 VSSSIKRN 68
 Db 56 IPSNEDHR 63
 RESULT 2
 BD04_BOVIN STANDARD; PRT; 63 AA.
 ID BD04_BOVIN
 AC P46162;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Beta-defensin 4 precursor (BNDS-4) (BNBD-4).
 GN DEFB4 OR BNBD4.

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yount N.Y., Yuan J., Diamond G., Tarver A., McGuire P.A.,
 RA McCullough C., Cullor J.S., Bevins C.L., Selsted M.E.,
 RA "Molecular cloning and expression of an antimicrobial beta-defensin
 RT from bovine neutrophils. Characterization of BNBD-4 cDNA and genomic
 RT sequences and localization of the peptide to large granules of mature
 RT neutrophils."
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yount N.Y., Yuan J., Tarver A.P., Diamond G., Levy J.N.,
 RA McGuire P.A., McCullough C., Cullor J.S., Bevins C.L., Selsted M.E.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Yount N.Y., Yuan J., Tarver A.P., Diamond G., Levy J.N., McGuire P.A.,
 RA McCullough C., Cullor J.S., Bevins C.L., Selsted M.E.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Ryan L.K., Rhodes J., Bhat M., Diamond G.,
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 23-63
 RC STRAIN=Hersford; TISSUE=Neutrophils;
 RX MEDLINE=93203264; PubMed=8454635;
 RA Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
 RA Smith W., Henschen A.H., Cullor J.S.;
 RT "Purification, primary structures, and antibacterial activities of
 RT beta-defensins, a new family of antimicrobial peptides from bovine
 RT neutrophils."
 RL J. Biol. Chem. 268:6641-6648 (1993).
 CC -1- FUNCTION: Has bactericidal activity. Active against E.coli ML35
 CC and S.aureus 502A.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neutrophilic granules.
 CC -1- SIMILARITY: Belongs to the beta-defensin family.
 CC
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 CC
 CC EMBL; U36200; AAD10283.1; -;
 CC EMBL; AF008307; AAB63292.1; -;
 CC EMBL; AF014107; AAD01522.1; -;
 CC HSP; P46170; 1BNB.
 CC InterPro; IPR001855; Defensin beta.
 CC InterPro; IPR006080; Defensin mammal.
 CC Pfam; PF00711; Defensin beta; 1.
 CC SMART; SM00048; DEFGN; 1.
 KW Antibiotic; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 22
 FT CHAIN 23 63 BETA-DEFENSIN 4.
 FT MOD_RES 23 23 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 31 60 BY SIMILARITY.
 FT DISULFID 38 53 BY SIMILARITY.
 FT DISULFID 43 61 BY SIMILARITY.
 SQ SEQUENCE 63 AA; 7161 MW; 3A4427EF57D654A3 CRC64;
 Query Match 19.8%; Score 75; DB 1; Length 63;
 Best Local Similarity 36.8%; Pred. No. 0.018;
 Matches 21; Conservative 5; Mismatches 29; Indels 2; Gaps 2;

QY 5 LLFAVFFCLVQNSGDIPPGIRN-TVCFMQRGCHLFMCESGERKGDICSDPNRCC 60
DB 6 LLLAVLFLVLSAGS-FTQVRNPOSCKRWGMVCPFLCRVGMQRIGTGFGRVPC 61

RESULT 3
D120 HUMAN
ID D120 HUMAN STANDARD; PRT; 88 AA.
AC Q8N659,
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-defensin 120 precursor (Beta-defensin 20) (DEPB-20).
GN DEPB120 OR DEPB20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND IDENTIFICATION.
RX TISSUE=B-cell, Fetal lung, and Testis;
MEDLINE=21843921; PubMed=11854508;
RA Schutte B.C., Mitros J.P., Bartlett J.A., Walters J.D., Jia H.P.,
RT Welsh M.J., Casavant T.L., McCray P.B. Jr.;
RT "Discovery of five conserved beta-defensin gene clusters using a
computational search strategy."
RL Proc. Natl. Acad. Sci. U.S.A. 99:2129-2133(2002).
CC -!- FUNCTION: Has antibacterial activity (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the beta-defensin family.
CC
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CC
CC EMBL; AY122473; AM93915.1; --
DR Genew; HGNC:18100; DEFB120.
KW Antibiotic; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 88 BETA-DEFENSIN 120.
FT DISULFID 23 49 BY SIMILARITY.
FT DISULFID 29 43 BY SIMILARITY.
FT DISULFID 33 50 BY SIMILARITY.
SQ SEQUENCE 88 AA; 10107 MW; BFFB1573ACF71C7 CRC64;

Query Match 19.5%; Score 74; DB 1; Length 88;
Best Local Similarity 33.3%; Pred. No. 0.033;
Matches 21; Conservative 9; Mismatches 23; Indels 10; Gaps 4;
QY 1 MKVLLFAVFFCLVQNSGDIPPGIRN-TVCFMQRGCHLFMCESGERKGDICSDPNRCC 60
DB 1 MKLLYFLAILAIEB-----PVISVECWMD-GHCRL-LCKDGEDSIIRCNR-KRCC 50

QY 61 VSS 63
DB 51 VPS 53

RESULT 4
BD01 CAPHI
ID BD01 CAPHI STANDARD; PRT; 64 AA.
AC Q97946;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta-defensin 1 precursor (BD-1).
GN DEFB1.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RX MEDLINE=20002622; PubMed=10531296;
RA Zhao C., Nguyen T., Liu L., Shamova O., Brogden K., Lehrer R.I.;
RT "Differential expression of caprine beta-defensins in digestive and
RT respiratory tissues."
RL Infect. Immun. 67:6221-6224(1999).
CC -!- FUNCTION: Has bactericidal activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the beta-defensin family.
CC
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CC
CC EMBL; Y17679; CAAY6811.1; --
DR HSSP; P46170; IBSB.
DR InterPro; IPR001855; Defensin beta.
DR InterPro; IPR006080; Defensin mammal.
DR Pfam; PF00711; Defensin beta_1.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 26
FT CHAIN 27 64 BETA-DEFENSIN 1.
FT DISULFID 31 60 BY SIMILARITY.
FT DISULFID 38 53 BY SIMILARITY.
FT DISULFID 43 61 BY SIMILARITY.
SQ SEQUENCE 64 AA; 7258 MW; 492B824C8F57B042 CRC64;

Query Match 19.0%; Score 72; DB 1; Length 64;
Best Local Similarity 33.3%; Pred. No. 0.042;
Matches 19; Conservative 7; Mismatches 29; Indels 2; Gaps 2;
QY 5 LLFAVFFCLVQNSGDIPPGIRN-TVCFMQRGCHLFMCESGERKGDICSDPNRCC 60
DB 6 LLLVFLVLSAGS-FTQGISSRRSCHRNGKVCALTRCPNRRQIGTGFGRVPC 61

RESULT 5
D118 MACMU
ID D118 MACMU STANDARD; PRT; 123 AA.
AC Q95LI0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-defensin 118 precursor (Epididymal secretory protein 13.6)
(ESP13.6).
GN DEFB118 OR ESC42.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis;
RX MEDLINE=21448442; PubMed=11564719;
RA Liu Q., Hamil K.G., Sivashamugam P., Grossman G., Soundararajan R.,
RA Rao A.J., Richardson R.I., Zhang Y.L., O'Rand M.G., Petrusz P.,
RA French F.S., Hall S.H.;
RT "Primate epididymis-specific proteins: characterization of ESC42, a
RT novel protein containing a trefoil-like motif in monkey and human."
RL Endocrinology 142:4529-4539(2001).
CC -!- FUNCTION: Has antibacterial activity (Potential).

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: High-level and epididymis-specific expression.
CC Most abundant in the epithelium of the caput and is also present
CC in the lumen and bound to sperm.
CC -!- SIMILARITY: Belongs to the beta-defensin family.
CC
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CC
CC EMBL; AF207834; AAL26779.1; -
CC GO; GO:0005653; C:perinuclear space; NAS.
CC GO; GO:0003797; F:antibacterial peptide activity; TAS.
CC GO; GO:0007160; P:cell-matrix adhesion; NAS.
CC GO; GO:0045087; P:innate immune response; TAS.
CC GO; GO:0007283; P:spermatogenesis; NAS.
CC KW Antibiotic; Signal.
CC FT SIGNAL 1 19 POTENTIAL.
CC FT CHAIN 20 62 BETA-DEFENSIN 118.
CC FT PROPEP 65 123 POTENTIAL.
CC FT DISULFID 27 54 BY SIMILARITY.
CC FT DISULFID 34 48 BY SIMILARITY.
CC FT DISULFID 38 55 BY SIMILARITY.
CC SQ SEQUENCE 123 AA; 13629 MW; E80EP33715FP94E1 CRC64;
Query Match 18.9%; Score 71.5; DB 1; Length 123;
Best Local Similarity 32.4%; Pred. No. 0.092;
Matches 22; Conservative 10; Mismatches 31; Indels 5; Gaps 3;
QY 1 MKVLLFAVFCVQVNSGDIIPGIRNTVCFMQRGCHRLFCMSRGERKGDICSDPWNRC 60
DB 1 MKLLALPILVLLPQ---VIPAYGSKKCNRSRSHCRK-QCKDGEAVKTCRN-HRACC 55
QY 61 VSSSIKNR 68
DB 56 VPSNEDR 63
RESULT 6
BD09_BOVIN STANDARD; PRT; 55 AA.
AC P46167; O18814;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-defensin 9 precursor (BNBD-9) (BNBD-9) (Fragment).
GN DBF9 OR BNBD9.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=98147718; PubMed=9488394;
RA Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
RA Erdjument-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
RA Wines M., Hwang S., Bevins C.L.;
RA "Enteric beta-defensin: molecular cloning and characterization of a
RT gene with inducible intestinal epithelial cell expression associated
RT with Cryptosporidium parvum infection."
RL Infect. Immun. 66:1045-1056 (1998).
RN [2]
RP SEQUENCE OF 16-55.
RC STRAIN=Hereford; TISSUE=Neutrophils;
RX MEDLINE=93203264; PubMed=8454635;
RA Seasted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
RA Smith W., Henschen A.H., Cullor J.S.;

RT "Purification, primary structures, and antibacterial activities of
RT beta-defensins, a new family of antimicrobial peptides from bovine
RT neutrophils.";
RL J. Biol. Chem. 268:6641-6648 (1993).
CC -!- FUNCTION: Has bactericidal activity. Active against E.coli ML35
CC and S.aureus 502A.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neutrophilic granules.
CC -!- SIMILARITY: Belongs to the beta-defensin family.
CC
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CC
CC EMBL; AF016394; AAC48801.1; -
CC HSP; P46170; IBNB.
CC DR InterPro; IPR001855; Defensin beta.
CC DR InterPro; IPR006080; Defensin_mammal.
CC DR Pfam; PF00711; Defensin_beta; 1.
CC DR SMART; SM00048; DEFSN; 1.
CC KW Antibiotic; Signal; Pyrrolidone carboxylic acid.
CC FT NON TER 1 1
CC FT SIGNAL <1 1 POTENTIAL.
CC FT PROPEP 2 15 POTENTIAL.
CC FT CHAIN 16 55 BETA-DEFENSIN 9.
CC FT MOD RES 16 16 PYRROLIDONE CARBOXYLIC ACID.
CC FT DISULFID 24 53 BY SIMILARITY.
CC FT DISULFID 31 46 BY SIMILARITY.
CC FT DISULFID 36 54 BY SIMILARITY.
CC FT CONFLICT 48 48 A -> G (IN REF. 2).
CC SQ SEQUENCE 55 AA; 6049 MW; 48DAE6917DE366F2 CRC64;
Query Match 18.7%; Score 71; DB 1; Length 55;
Best Local Similarity 33.3%; Pred. No. 0.048;
Matches 18; Conservative 7; Mismatches 27; Indels 2; Gaps 2;
QY 8 AVFECVQVNSGDIIPGIRNTVCFMQRGCHRLFCMSRGERKGDICSDPWNRC 60
DB 2 ALLFLVLSAGSG-FTQGVRAVFTCRINRGFCVPCIRCFGHRHQICTCLAPQIKCC 54
RESULT 7
BD03_BOVIN STANDARD; PRT; 57 AA.
AC P46161;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-defensin 3 precursor (BNBD-3) (BNBD-3) (Fragment).
GN DBF3 OR BNBD3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=98147718; PubMed=9488394;
RA Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
RA Erdjument-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
RA Wines M., Hwang S., Bevins C.L.;
RA "Enteric beta-defensin: molecular cloning and characterization of a
RT gene with inducible intestinal epithelial cell expression associated
RT with Cryptosporidium parvum infection."
RL Infect. Immun. 66:1045-1056 (1998).
RN [2]
RP SEQUENCE OF 15-67.
RC STRAIN=Hereford; TISSUE=Neutrophils;

[illegible]

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DR	EWBL; U75250; AAB61995.1; --				
DR	HSPF; P46170; IBNB.				
DR	InterPro; IPR001855; Defensin_beta.				
DR	InterPro; IPR006080; Defensin_mammal.				
DR	Pfam; PF00711; Defensin_beta_1.				
DR	SMART; SMC0048; DEFSN; I.				
KW	Antibiotic; Signal.				
FT	SIGNAL	1	22		BY SIMILARITY.
FT	CHAIN	23	64		BETA-DEFENSIN 1.
FT	DISULFID	31	60		BY SIMILARITY.
FT	DISULFID	38	53		BY SIMILARITY.
FT	DISULFID	43	61		BY SIMILARITY.
SO	SEQUENCE	64 AA;	7244 NW;	3529A9B76ABD023A	CRC64;

```

Query Match      18.2%; Score 69; DB 1; Length 64;
Best Local Similarity 31.6%; Pred. No. 0.096;
Matches 18; Conservative 8; Mismatches 29; Indels 2; Gaps 2;
QY 5 LLFAVFCLVQRNSGDIPIRNTV-CFMORGHCKLFMCRSGERKIGDSCDPNRRCC 60
      : : : : :
Db 6 LLALVFPWLVSASGC-ETQVGRNLSCHRNKGVCPSCRPHRMQIGTCRGGPVKCC 61
      : : : : :

```

RESULT 10	
NUOS HUMAN	
ID INDS HUMAN	STANDARD; PRT; 87 AA.
C Q9NRX3;	
AT 28-FEB-2003 (Rel. 41, Created)	
DC 28-FEB-2003 (Rel. 41, Last sequence update)	
DT 10-OCT-2003 (Rel. 42, Last annotation update)	
DE NADH:ubiquinone oxidoreductase MLRQ subunit homolog (NUOMS).	
OS Homo sapiens (human)	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
NCBI_TaxID=9606;	
[1]	
RN SEQUENCE FROM N.A.	
RP	
RC TISSUE=Adrenal gland;	
RX MEDLINE=20402571; PubMed=10931946;	
RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,	
RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,	
RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,	
Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,	
RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;	
RT "gene expression profiling in the human hypothalamus-Pituitary-adrena-	
RT axis and full-length cDNA cloning."	
RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).	
[2]	

RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22338257; PubMed=12477932;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Suecwo K.H., Schaefer C.F.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleaton M., Soares M.B., Ronald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.W., Sodergren E.J., Tu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences."; [PMID: 11745454](#)
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
CC !- SIMILARITY: Belongs to the complex I NDUF44 subunit family.

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CC or send an email to license@isb-sib.ch).

CC	EMBL; AF164796; AAF80760.1; -
DR	EMBL; BC011910; AAH11910.1; -
SR	SEQUENCE 87 AA; 9966 MW; A08D7182A0A3C87 CRC64;

```

Query Match      18.1%; Score 68.5; DB 1; Length 87;
Best Local Similarity 29.9%; Pred. No. 0.15;
Matches 20; Conservative 11; Mismatch 27; Indels 9; Gaps 3;

QY      6  LFAVFCLVQRSGDIPPGIRNTVCFMQRGHCRLEWCRSGRKGDCISD-----PWNR 59
      : : : : : : : : : : : : : : : : : : : : : :
Db      6  LGARFYRQIKRHPGIIIP--MIGLIC-LGMSGAAVLRLRLALRSPDVCWDRKNNPEPWRL 62

QY      60  CVSSSIK 56
      : : : : :
Db      63  SPNDQYK 69

```

RESULT	11
ID	MYX3_CRODU
ITD	MYX3_CRODU STANDARD; PRF; 65 AA.
AC	P24333;
DT	01-MAR-1992 (Rel. 21, Created)
DD	01-MAY-1992 (Rel. 21, Last sequence update)
DE	10-OCT-2003 (Rel. 42, Last annotation update)
DG	Crotaxin 3 precursor (Crotamine 3).
DS	Crotaxin durissus terrificus (South American rattlesnake).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Lepidodactylia; Squamata; Scieroglossa; Serpentes; Colubroidae;
CC	Viperidae; Crotalinae; Crotalus.
RN	NCBI_TaxID=8732;
OX	[1]
SEQUENCE FROM N.A.	
TISSUE=Venom gland;	
MEDLINE=90357261; PubMed=2389256;	
Smitz L.A., Schmidt J.J.	
"Cloning and nucleotide sequences of crotamine genes."	
Toxicol 28:575-585(1990).	
-! FUNCTION:	Causes severe muscle necrosis by a non-enzymatic mechanism. Acts extremely rapidly and serves two primary functions: limit the flight of prey by causing instantaneous paralysis of the hind limbs and promote rapid death by paralyzing the diaphragm.
CC CC CC CC CC CC CC	

CC	or one diaphragm.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC	-1- SIMILARITY: Belongs to the snake toxin myotoxin family
DR	PIR; C35947; C35947.
DR	InterPro; IPR000881; Myotoxin.
DR	Pfam; PF00819; Myotoxins; 1.
DR	PRINTS; PR00283; MYOTOXIN.
DR	ProDom; PD005972; Myotoxin; 1.
DR	PROSITE; PS00459; MYOTOXINS; 1.
KW	Toxin; Signal.
FT	SIGNAL 1 22
FT	CHAIN 23 64
FT	DISULFID 26 58
FT	DISULFID 33 52
FT	DISULFID 40 59
SQ	SEQUENCE 65 AA; 7371 MW; AIBT5A6CCS15BA06 CRC64;

Query Match 17.8%; Score 67.5; DB 1; Length 65;

GN DEFBI103 OR DEFBI3 OR BD3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A., SEQUENCE OF 23-67, FUNCTION, TISSUE SPECIFICITY,
 RP INDUCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Keratinocytes, lung epithelial cells, and Tracheal epithelium;
 RX MEDLINE=21101950; PubMed=11085990;
 RA Harder J., Bartels J., Christophers E., Schroeder J.-M.;
 RT "Isolation and characterization of human beta-defensin-3, a novel
 RT human inducible peptide antibiotic.";
 RT J. Biol. Chem. 276:5707-5713(2001).
 [2]
 RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RP MEDLINE=2158153; PubMed=11702237;
 RX Garcia J.-R., Jaumann F., Schulz S., Krause A., Rodriguez-Jimenez J.,
 RA Forssmann U., Adernann K., Kluever S., Vogelmeier C., Becker D.,
 RA Hedrich R., Forssmann W.-G., Bals R.;
 RT "Identification of a novel, multifunctional beta-defensin (human
 RT beta-defensin 3) with specific antimicrobial activity. Its
 RT interaction with plasma membranes of *Xenopus* oocytes and the
 RT induction of macrophage chemotaxis.";
 RT Cell Tissue Res. 306:257-264(2001).
 [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21125233; PubMed=11223260;
 RX Jia H.P., Schutte B.C., Schudy A., Linzmeier R., Guthmiller J.M.,
 RA Johnson G.K., Tack B.F., Mitros J.P., Rosenthal A., Ganz T.,
 RA McCray P.B. Jr.;
 RT "Discovery of new human defensins using a genomics-based approach.";
 RT Gene 263:211-218(2001).
 [4]
 RN SEQUENCE FROM N.A.
 RP Inai Y.;
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RN SEQUENCE FROM N.A.
 RP Adler D.A., Diamond G., Sheppard P., Holloway J., Presnell S.,
 RA Jaepers S., Whitmore T., Fox B., Gosink J., Rixon M., Gao Z.,
 RA Haldeman B., O'Hara P.;
 RT "EST and genomic database mining yield novel human and mouse
 RT beta-defensins.";
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RN STRUCTURE BY NMR OF 23-67.
 RX MEDLINE=21864161; PubMed=11741980;
 RA Schibli D.J., Hunter H.N., Asyev V., Starner T.D., Wiencek J.M.,
 RA McCray P.B. Jr., Tack B.F., Vogel H.J.;
 RT "The solution structures of the human beta-defensins lead to a better
 RT understanding of the potent bactericidal activity of HBD3 against
 RT *Staphylococcus aureus*.";
 RT J. Biol. Chem. 277:8279-8289(2002).
 [7]
 CC -1- FUNCTION: Exhibits antimicrobial activity against Gram-positive
 CC bacteria *S.aureus* and *S.pyogenes*, Gram-negative bacteria
 CC *P.aeruginosa* and *E.coli* and the yeast *C.albicans*. Kills
 CC multiresistant *S.aureus* and vancomycin-resistant *E.faecium*. No
 CC significant hemolytic activity was observed.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in skin and tonsils, and to a
 CC lesser extent in trachea, uterus, kidney, thymus, adenoid, pharynx
 CC and tongue. Low expression in salivary gland, bone marrow, colon,
 CC stomach, polyp and larynx. No expression in small intestine.
 CC -1- INDUCTION: By infection of bacteria and by interferon gamma.
 CC -1- MASS SPECTROMETRY: MW=5154.59; METHOD=Electrospray; RANGE=23-67.
 CC -1- SIMILARITY: Belongs to the beta-defensin family.
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 CC -----
 CC DR EMBL; AJ237673; CAC03097.1; -
 CC DR EMBL; AF295370; AAG02237.1; -
 CC DR EMBL; AF217245; AAF73853.1; -
 CC DR EMBL; AB037972; BAB40572.1; -
 CC DR EMBL; AF301470; AAG22030.1; -
 CC DR PDB; 1KJ6; 20-MAR-02.
 CC DR Genew; HGNC:15967; DEFB103.
 CC DR MN; 606811; -
 CC DR GO; GO:0005576; C:extracellular; NAS.
 CC DR GO; GO:0008224; F:anti-Gram-positive antibacterial peptide activity; TAS.
 CC DR GO; GO:0006965; P:anti-Gram-positive bacterial polypeptide in.; TAS.
 CC DR InterPro; IPR001855; Defensin_beta_1.
 CC DR Pfam; PF00711; Defensin_beta_1.
 CC DR Antibiotic; Signal; 3D-Structure.
 CC KW SIGNAL 1 22
 CC FT CHAIN 23 67 BETA-DEFENSIN 103.
 CC FT DISULFID 33 62
 CC FT DISULFID 40 55
 CC FT DISULFID 45 63
 CC SQ SEQUENCE 67 AA; 7697 MW; 54266DE1C90D4B65 CRC64;
 CC Query Match 17.4%; Score 66; DB 1; Length 67;
 CC Best Local Similarity 31.7%; Pred. No. 0.23;
 CC Matches 19; Conservative 8; Mismatches 27; Indels 6; Gaps 2;
 CC -----
 CC QY 5 LLFVFFCLVQNSGDIPPGIRNTV---CFMORGHCLFMCRSGERKGDICSDPWNRCC 60
 CC Db 6 LLFALLFLFVFPFH---GGIINTLQKYKVRGRCANVLSCLPKEQIGKSTRGRKCC 63
 CC -----
 CC RESULT 15
 CC DEF1 MACMU
 CC ID DEF1 MACMU STANDARD; PRT; 96 AA.
 CC AC P60030; P82318;
 CC DT 15-MAR-2004 (Rel. 43, Created)
 CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC DE Neutrophil defensin 1 precursor (RMAD-1).
 CC OS Macaca mulatta (Rhesus macaque).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC OC Cercopithecinae; Macaca.
 CC OX NCBI_TaxID=9544;
 CC [1]
 CC RN SEQUENCE FROM N.A., SEQUENCE OF 67-96, AND MASS SPECTROMETRY.
 CC RP TISSUE=Bone marrow, and Leukocytes;
 CC RX MEDLINE=2002603; PubMed=10531277;
 CC RA Tang Y.Q., Yuan J., Miller C.J., Selsted M.E.;
 CC RT "Isolation, characterization, cDNA cloning, and antimicrobial
 CC RT properties of two distinct subfamilies of alpha-defensins from rhesus
 CC RT macaque leukocytes.";
 CC RL Infect. Immun. 67:6139-6144(1999).
 CC -1- FUNCTION: Has bacteriostatic activity against Gram-positive
 CC bacteria *S.aureus* and *L.monocytogenes* and Gram-negative bacterium
 CC *E.coli* and antifungal activity against *C.neoformans*. Has
 CC microbicidal activity against Gram-positive bacteria *S.aureus* and
 CC *L.monocytogenes*.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=3446.9; METHOD=MALDI; RANGE=67-96.
 CC -1- SIMILARITY: Belongs to the corticostatin/defensin family.
 CC -----
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CC EMBL; AF188268; AAF06312.1; -

DR PIR; A59076; A59076.
DR HSP; P11479; IDPN.
DR InterPro; IPR006081; Defensin_alpha.
DR InterPro; IPR006080; Defensin_mammal.
DR InterPro; IPR002386; Defensin_propep.
DR Pfam; PF00323; defensins; 1.
DR Pfam; PF00879; Defensin_propep; 1.
DR SMART; SM00048; DEFSN; 1.
DR PROSITE; PS00269; DEFENSIN; 1.
KW Defensin; Antibiotic; Fungicide; Signal.
FT SIGNAL 1 19
FT PROPEP 20 66
FT CHAIN 67 96
FT DISULFID 68 95
FT DISULFID 70 85
FT DISULFID 75 96
SQ SEQUENCE 96 AA; 10544 MW; BDC8A81AD8E304C5 CRC64;

Query Match 17.3%; Score 65.5; DB 1; Length 96;
Best Local Similarity 35.6%; Pred. No. 0.38;
Matches 16; Conservative 5; Mismatches 15; Indels 9; Gaps 3;

QY 20 DTPPGIR-NTVCFMQRGHCRFLPWCERSGERKGDIC---SDPWNRC 60
DB 57 DSVPGLRKNMACY-----CRIPACLAGERRYGTCTFYLGKRWAFCC 96

Search completed: June 14, 2004, 16:39:32
Job time : 15 secs